

Table 70: Comparative Sequences relating to SAG 1280

ATACCTTTATTGAGTTTGAAACCTTGAATTTGATTTCTTTTGTGGATGAGGCTCATC
 ACTTCAAGAAATATCCGTCCAATCACTGGACTTGGGAATGTAGCTGGAATCACCACACAA
 CTTCTAAAAAGAACGTTGGATATGGAGATGAAGGTGAGACAGTACAGGCAGAGCATGGAG
 ATAGAAATGTCTGTTTTCGACAGGAACACCAAGTTTCTAACTCTATTAGTGAACCTTTCA
 CCATGATGGATTACATTCAACCTGATGTCTTGGAACGATACCTGGTATCAAAATTTGACT
 CCTGGGTTGGGGCTTTTGGGAATATCGAAACTCCATGGAAGTACCCCGACAGGAGATA
 AGTACCAACCCAGAAACGTTCAAGAAATTTGTCAACCTTCCTGAACTCATGCGAATCT
 ACAAGGAACTGCCGATATTAGACCTCAGACATGCTTGATTACACAGTACCGGAAGCTA
 AGATTATTGCGGTGGAAGCGAGTTAACGCAAGCTCAGAAATACTATTGGAAGAGCTGG
 TAAAGCGTTGACAGCGTATCAAGTCAGGTAGTGTGATCCAAGTAGAGATAACATGCTTA
 AAATCACAGGAGAAGCCAGAAACTAGCTATTGATATGCGGTTGATTGACCCCTACTTACT
 CCTTATCGGATAATCAGAAATCCTTCAAGTAGTTCGATAATGTCGAGCGGATTACCGTG
 ATGGAGCTGGAGACAAGCCACTCAGATGATTCTCAGATATTGGAACCCCTAAAAGTA
 AGGAAGAAGGGTTTGATGTCTACAATGAACCTTAAGGACTTGTTTGTGCGATCGAGGGATAC
 CAAAAGAGAAATTTGCTTCCATGATGCCAATCTGATGAGAAGAAAACTCTCTGT
 CAGCAAGGTCAATAGTGGAGAAAGTACGGATTCTCATGGCTTCTACGGAAGAAAGGGGAA
 CAGGATTAACCTCCATCTCGCATGAAAGCTGTCCACTATTAGACGTTCCCTGGAGGC
 CCTCAGACATTGTCCAGCGAAATGGACGACTAATTCGACAAGGAAACATGCACCGAGG
 TAGATATTATCACTATTACTAAAGGGAGCTTTGACAATTACCTCTGGCAGACGCGAG
 AGAATAAGCTAAAGTATATCACCCAGATAATGACCTCAAAGATCCTGTGAGATCAGCTG
 AAGACATTGATGAACAAACCATGACCGCTCAGACTTAAAGGCATTGGCAACTGGGAACC
 CTTATCTCAAACCTCAAATGGAGTTGGAAATGAACCTGACAGTTTATAGAGAACTCAAAC
 GAGCCTTTAATCGCTCCAAAGACGAGTATCGCCATACCATTTCTATAGCGAGAAGCACC
 TCCTTATTATGGAAGAACGTTGAGTCAATATGATAAAGATATTGCCCAATCTTTGGCAA
 CCAAGTCGCAAGATTTTGTGATGCGATTGACAATCAAGCAATGGATAATCGTGCTGAAG
 TGGGGACTATCTGCGAAACCTATTACCTATAACCGCTCAGAGACCAAGGAAGTCAGGA
 CACTTGGCAGCTTTAGAGGATTTGATTAAAAATGACTACACGAGGTGCTAGTGAGCCCT
 TACCAGAAACCATTTCTTAAATGATTGATGGTATACACAGTATCTGTGCGCCCTTGATT
 TGAATACAGACCTGGGAACCATTCACCGATTAGTAATGCCATTGACCATATTATAGATG
 ACCAAGAAAGACGCAAGAGCTGGTAAAGGATTTAAAGATAAGCTACAGGTAGCCAAAG
 TAGAAGTTGATAAAGTCTTTCCAAAGGAAGAGGACTATCAGCTTGTAAGGCTAAGTATG
 ATGTTTATGCTCCCTTGGTTGAAAAGAGAGCAGAGATTGAAGAGATAGATGCAGCTTTGG
 CCAAGTTTAGTGAAGATACAACCCCAAGGAAGCAACAAATAGCATTGCGAGATA

SEQ ID. NO. 7002

STRAIN H36B

GGAGGGAAAATGAATCAAGAAGTCTTACTACAAATGAT
 GAGAGCCACTATTCCTCGTGATAGAGCCCTTGCTTGAGGCATTTTATATT
 ACCAAGCAGAGCATTTTGTGATGAGGAGTGGGATAGTCTTATTCATCAGTTT
 ATGACCAATAGGCAAGAAATAAATAAGTCTGTTCAAGTACTTCACTTTGA
 GACAGATGTTTCACTTTTGTCCAGGCTAGTCTTATGATAGTCTCATG
 ATCTATTGACCTATACACAAGTTTTCGGCCAAAGTGGTCTTCAAAAATA
 GATAAATATCGCCGCTGAAAAAACTTGGTGATAGAAGTGGCCTTGT
 CAATCTGGCCACTCGTTTCAATTATTGGATTCCAATGGACACTACCAA
 CCATATCGCCGATTCACTCTTACAAAAGAGTAGGGAGCTAATTGGTC
 AATGTGTATCGTGTGGCTAATAATTAGCGGATCGTATTAGTTCGAGATAT
 TGAACAGTTTCTCTAACTTACGAGCCTGAGCTTGAACTAGAGCTGATG
 AAAGTGTCTAGAAAAATGAAGAACTGTGATGAGCACAAAAAGTGT
 CATCAAGCAATATCTTTGAGAAGAGGGCTCTCTGTTATTGCTAGTTT
 GGATGTAGATTGTCTCAACTAGATGTTCAAAATAGGAAAAACAGTCTATC
 TGCCAGCTTATGAAGAGTTATCCTTACGACGTAATTTGAGATTCTAACA
 TATTTTGACCAAAATCGAAATGAACGTTCCAAAGTCCCAAGTTTATAGC
 AGGTGATTTTGACACAGAGATGGAAATGACACAGTCTTTGATGGCGAGG
 AATTACTTACTTATCTCGAAGCTGATGGCAGTCCCTATGAGCTGAAACGA
 ACGCTGACTACAGTCAAGAAAAAGGAATTAGAAAAAATGGACAAGCCAT
 TAGGATAGAAAAATCAAGAAAAATGACTCAGCTA₈GkATTGrTTTATCTC
 AGTTTGACCCAGACCGAGTCCGTTATTTATTGkATGCAGCAGGTCTGTT
 CGTTT_{Aw}AwAATGACAGCTTGTCTCACTAGGTGGTTATCCAAAGCCTC
 GGTAACTCACTAGCCCTTGCGACAGAACTACTCCAAATGGGACTAAGTC
 ATGAAAAGGTTGAATTTTCTTTGGTAGCCAGCTTCCATGGAAGAGCTG
 CGACAAGTTGCCTACGCCCTTTTACACCAAGAACTCAGCAGAGAAGATGC
 GGAGCAATTTGAAAAAGATAAAGGTAATCAGCCAGATTAACTCTCAGAG
 ATTGGAAAAGCAAGCTAGAGAAAGCTGAGGGAAAAGAGTAGTTGATGAA
 GAATTCGCGGAAAATCCACTGGTTGAGAGATATTGGACACTTATCCTCT
 GGGGTCAATTGGTTTCTATAAGGGACAGGACTTTGAGGTCTGTCGCTCA
 GCGATGCTCGATGAACGGTTTGATTGCGATTGAGTTAGTCAATGACTTT
 TCGGATATCATTGAACAAAATCCAGTTCTTTATGTGAGGACCTGGGAAGA
 AGTCAGTCAGGCACTTCATCAGCCAAAGGCAGAACCAAAACAGAGTTAG
 AAGAAGCGGACCAAGAATTAAACCTATTCTCATTTCTGGAAGAGGAGCTA
 GTTCAGAGTATTGGACTATTGGAAACAGATGATTAGAAAAATGGTCATAA
 CGATACTGATCTTGAAGAAACAGATAATCAAAATTCCTGAAGAGGAAGTCG
 TCGAAACAATTCAGAGATTCCAGTAAACGGACTTTTATTTTCAGAAAGAT
 TTGACGGACTTTTATCCTAAGACTGCTAGAGATAAGTTGAGACAAACAT
 TGTGGCCATTGTTTGGTAAAAATCTAGAAGTAGAGCACCGCAATGCTT
 CACCAAGTGAACAAAGAACTCTTGCCAAGTATGAGGCTGGGGTGGACTA
 GCCAATGAATTTTGTGACTATAATCCAAATTTTCTAAGGAACGAGA
 AGAAGTGAAGAGCTAGTCAAGATAAAGAGTATTGCGATATGAACAGT
 CCTCCCTGACAGCCTATTACACAGACCCATCCCTGATCCGTGAGATGTGG
 GATAAGTTGGAAGAGATGGCTTTACAGGTGGCAAAATCCTAGATCCTTC
 CATGGGAACAGGGAATTTCTTTGCGGCTATGCCAAAACACTTAAGAGAAA
 AGAGTGAGTTGATGGCGTAGAGTTAGATACTATTACAGGAGCTATTGCC
 AAACACCTTCATCCCAATAGTCATATTGAATTAAGGGATTTGAGACGGT
 GGCTTTTAAACGCAATAGTTTGGATTGGTGATTCAAATGTGCCCTTTG

Table 70: Comparative Sequences relating to SAG 1280

CCAATATACGAATTGCGGATAATAGGTACGATAGGCCCTTACATGATTTCAT
 GACTACTTTGTCAAAAAGTCACTTGATTTGCTTCATGATGGTGGACAAAGT
 AGCGATTATCTCTTCCACAGGAACATATGGATAAGCGAACAGAAAACATCT
 TACAAGATATTCTGAGACAACCTGAATTTCTTGGTGGGGTTCGACTGCCT
 GACTCTGCCCTTAAGGCCATTGACAGGAACGAGTGTCAACACGGATATGTT
 ATTCTTCCAGAAACACTTAGACAAGGGATATGTGGCAGACGATTTAGCCT
 TTTGAGTTCCATTCGCTATGACAAGGATAGTCGCATTTGGCTCAATCCT
 TATTTTGATGGAGAATACAATAGCCAGGTGCTAGGAACCTACGAGGTGAG
 GAATTTTAACGGAGGAACACTTTCTGTTAAGGGGACTAGTGATGACTTGA
 TTGCAAGTGTGAAACAGCTCTAAATCACGTTAAGGCCCAAGAGAGATT
 GATAGAAATGAGGTCACTTAACCCAGATGTGTTGACCAACAAGTCAA
 TGATACCTCCATTCCAGCTGAAATGAGGGAAAATCTAGGTGAGTACAGTT
 TTGGTTATCAGGGGTCTACAGTTTACTATCGAGATAACAAAGGCATTGGA
 GTCGGAACCAAGACGGAAGAAATCAGTTACTATGTCGATGAAGAG

SEQ ID. NO. 7003

STRAIN 18RS21

GnAGGGAAAATGAATCAAGAAGTCTTACTACAAATGATGAGA
 GCCACTATTCTCGTGATAGAGCCTTGCTTGAGGCATTTTATATTACCA
 AGCAGAGCATTTTGATGAGGAGTGGGATAGTCTTATTTCATCAGTTTATGA
 CCAATAGGCAAGAAAATAAATAGTCTGTTCAAGTACTTCACTTTGAGACA
 GATGTTTCAGCTTTTGTCCAGGCTAGTCTTATGATACTGCTCATGATCT
 ATTGACCTTATACACAAGTTTTCGGCCAAAGTGGTCTTCAAAAACCTAGATA
 AACTATCGCCGCTGAAAAAACTTGGTGATAGAAGTGGCCTTGTTCAT
 CTGGCCACTCGTTTCAATTTATGGATTCCAATGGACACTACCAACCAT
 ATCGCCGATTCACTCTTACAAAAGAGTAGGGGAGCTAATTTGGTCAATG
 TGTATCGTGTGGCTAATAATTTAGCGGATCGTATTAGTCGAGATATTGAA
 CAGTTTCTCTTAACCTTACGAGCCTGAGCTTGAAACTAGAGCTGATGAAAC
 TGTCTAGAAAAATGAAGAACTGTTGATGAGCACAACAAAGTGTTCATC
 AAGCAATATCTTTTCGAGAAGAGGGCTCTCTGGTTATTGCTAGTTTGGAT
 GTAGATTTGTCTCACTAGATGTTCAAATAGGAAAAACAGTCATCTGCC
 AGCTTATGAAGAGTTATCCTTACGAGCTAAATTTGAGATTCTAACATATT
 TTGACCAAAATCGAAATGAACGTTCCAAAGTCCCAAGTTTGTAGCAGGTT
 GATTTTGACACAGAGATGGAATGACACCAAGTCTTTGATGGCGAGGAATT
 ACTTACTTATCTCGAAGCTGATGGCAGTCCCTATGAGCTGAAACGAACGC
 TGACTACAGTcGAAGAAAAGGAATTAGAAAAAATTTGGACAAGCCATTAGG
 ATAGAAAAATCAAGAAAAATGACTCAGCTAGGGATTGATTTATCTCAGTT
 TGACCCAGACCGAGTCCGTTATTTTATTTGGATGACAGGTCGTTTTCGTT
 TAAAAAATGACAGCCTTGCTTTACTAGGTGGTTATCCCAAAGCCTCGGTA
 ACTCAACTAGCCCTTGCAGACAGAACTACTCCAATGGGACTAAGTCATGA
 AAAGGTTGAATTTTCTTTGGTAGCCAGCTTTCCATTGAAGAGCTGCGAC
 AAGTTGCCCTACGCCCTTTTACACCAAGAACTCAGCAGAGAAGATGCGGAG
 CAATTTGAAAAAGATAAAGGTAATCAGCCAGATTAACTCTCAGAGATTG
 GAAAGCAAGCTAGAGAAAGCTGAGGGAAAAGAGTAGTTGATGAAGAAT
 TCGCGGAAAATCCACTGTTTCAAGAGTATTGGACACTTATCCTCTGGGG
 TCATTGGTTTCTTATAAGGGACAGGACTTTGAGGTCAATGTCGGTCAAGCA
 TGCTCGATTGAACGGTTTGATTTCGGATTGAGTTAGTCAATGACTTTTCG
 ATATCATTGAACAAAAATCCAGTTCTTATGTGAGGACCTGGGAAGAAAGTC
 AGTCAGGCACTTCATCAGCCAAAGGCAGAACCAAAACAGAGTTAGAAGA
 AGCGGACCAAGAATTAAACCTATTCTCATTCTGGAAGAGGAGCCAGTTT
 AGAGTATTGGACTATTGGAACCAAGATGATTGAGAAAATGGTTCATAACGAT
 ACTGATCTTGAAGAAACAGATAATCAAATTCCTGAAGAGGAAGTCTGCGA
 AACAAATCCAGAGATTCCAGTAACGGACTTTTATTTTCCAGAAGATTGA
 CGGACTTTTATCTAAGACTGCTAGAGATAAGGTTGAGACAAACATTGTG
 GCCATTCTGTTGGTAAAAATCTAGAAGTAGAGCACCAGCAATGCTTCACC
 AAGTGAAACAAGAACTCCTTGCCAAGTATGTAGGCTGGGGTGGACTAGCCA
 ATGAAATTTTGTGATGACTATATCCAAAATTTTCTAAGGAACAGAGAAGAA
 CTGAAGAGCCTAGTCAAGATAAAGAGTATTCCGATATGAACAGTCCCTC
 CCTGACAGCCTATTACACAGACCCATCCCTGATCCGTGAGATGTGGGATA
 AGTTGGAAGAGATGGCTTTACAGGTGGCAAAATCTTAGATCCTTCCATG
 GGAACAGGGAATTTCTTTCGGCTATGCCCCAACACTTAAGAGAAAAGAG
 TGAGTTGTATGGCGTAGAGTTAGATACTATTACAGGAGCTATTGCCAAAC
 ACCTTTCATCCCAATAGTCATATTGAAATTAAGGGATTGAGACGGTGGCT
 TTTAACGACAATAGTTTGAATTTGGTGATTTCAAATGTGCCCTTTTGCCAA
 TATACGAATTGCGGATAATAGGTACGATAGGCCCTTACATGATTTCATGACT
 ACTTTGTCAAAAAGTCACTTGATTGCTTTCATGATGGTGGACAAGTAGCG
 ATTATCTCTTCCACAGGAACATATGATAAGCGAACAGAAAACATCTTACA
 AGATATTCTGAGACAACCTGAATTTCTTGGTGGGGTTCGACTGCCCTGACT
 CTGCCCTTAAGGCCATTGACAGGAACGAGTGTCAACACGGATATGTTATT
 TTCCAGAAACACTTAGACAAGGGATATGTGGCAGACGATTTAGCCTTTTC
 AGGTTCCATTTCGCTATGACAAGGATAGTCGCATTTGGCTCAATCTTATT
 TTGATGGAGAATACAATAGCCAGGTGCTAGGAACCTACGAGGTGAGGAAT
 TTTAACGGAGGAACACTTTCTGTTAAGGGGACTAGTGATGACTTGATGTC
 AAGTGTGAAACAGCTCTAAATCACGTTAAGGCCCAAGAGAGATTGATA
 GAAATGAGGTCACTTAACCCAGATGTGTTGACCAACAAGTCAATGAT
 ACCTCCATTCCAGCTGAAATGAGGGAAAATCTAGGTGAGTACAGTTTGG
 TTATCAGGGGTCTACAGTTTACTATCGAGATAACAAAGGCATTGAGTGC
 GAACCAAGACGGAAGAAATCAGTTACTATGTCGATGAAGAG

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa31161.2{*} June 20, 2002 10:41 ..

Table 70: Comparative Sequences relating to SAG 1280

msa31161.2{327dnt_2603}	GgAGGGAAAA	TGAATCAAGA	AGTCTTACTA	CAAATGATGA	GAGCCACTAT
msa31161.2{327d_18RS21}	GnAGGGAAAA	TGAATCAAGA	AGTCTTACTA	CAAATGATGA	GAGCCACTAT
msa31161.2{327dnt_H36B}	GgAGGGAAAA	TGAATCAAGA	AGTCTTACTA	CAAATGATGA	GAGCCACTAT
Consensus	*-*****	*****	*****	*****	*****
	51				100
msa31161.2{327dnt_2603}	TCCTCGTGAT	AGAGCCTTGC	TTGAGGCATT	TTTATATTAC	CAAGCAGAGC
msa31161.2{327d_18RS21}	TCCTCGTGAT	AGAGCCTTGC	TTGAGGCATT	TTTATATTAC	CAAGCAGAGC
msa31161.2{327dnt_H36B}	TCCTCGTGAT	AGAGCCTTGC	TTGAGGCATT	TTTATATTAC	CAAGCAGAGC
Consensus	*****	*****	*****	*****	*****
	101				150
msa31161.2{327dnt_2603}	ATTTTGATGA	GGAGTGGGAT	AGTCTTATTC	ATCAGTTTAT	GACCAATAGG
msa31161.2{327d_18RS21}	ATTTTGATGA	GGAGTGGGAT	AGTCTTATTC	ATCAGTTTAT	GACCAATAGG
msa31161.2{327dnt_H36B}	ATTTTGATGA	GGAGTGGGAT	AGTCTTATTC	ATCAGTTTAT	GACCAATAGG
Consensus	*****	*****	*****	*****	*****
	151				200
msa31161.2{327dnt_2603}	CAAGAAATAA	ATAAGTCTGT	TCAAGTACTT	CACITTTGAGA	CAGATGTTTC
msa31161.2{327d_18RS21}	CAAGAAATAA	ATAAGTCTGT	TCAAGTACTT	CACITTTGAGA	CAGATGTTTC
msa31161.2{327dnt_H36B}	CAAGAAATAA	ATAAGTCTGT	TCAAGTACTT	CACITTTGAGA	CAGATGTTTC
Consensus	*****	*****	*****	*****	*****
	201				250
msa31161.2{327dnt_2603}	AGCITTTGTC	CAGGCTAGTC	CTTATGATAC	TGCTCATGAT	CTATTGACCT
msa31161.2{327d_18RS21}	AGCITTTGTC	CAGGCTAGTC	CTTATGATAC	TGCTCATGAT	CTATTGACCT
msa31161.2{327dnt_H36B}	AGCITTTGTC	CAGGCTAGTC	CTTATGATAC	TGCTCATGAT	CTATTGACCT
Consensus	*****	*****	*****	*****	*****
	251				300
msa31161.2{327dnt_2603}	ATACACAAGT	TTTCGGCCAA	AGTGGTCTTC	AAAACTAGA	TAAACTATCG
msa31161.2{327d_18RS21}	ATACACAAGT	TTTCGGCCAA	AGTGGTCTTC	AAAACTAGA	TAAACTATCG
msa31161.2{327dnt_H36B}	ATACACAAGT	TTTCGGCCAA	AGTGGTCTTC	AAAACTAGA	TAAACTATCG
Consensus	*****	*****	*****	*****	*****
	301				350
msa31161.2{327dnt_2603}	CCGTCCTGAAA	AAAACCTGGT	GATAGAAGTG	GCCTTGTTCA	ATCTGGCCAC
msa31161.2{327d_18RS21}	CCGTCCTGAAA	AAAACCTGGT	GATAGAAGTG	GCCTTGTTCA	ATCTGGCCAC
msa31161.2{327dnt_H36B}	CCGTCCTGAAA	AAAACCTGGT	GATAGAAGTG	GCCTTGTTCA	ATCTGGCCAC
Consensus	*****	*****	*****	*****	*****
	351				400
msa31161.2{327dnt_2603}	TCGTTTTCAA	TTATTGGATT	CCAATGGACA	CTACCAAACC	ATATCGCCGG
msa31161.2{327d_18RS21}	TCGTTTTCAA	TTATTGGATT	CCAATGGACA	CTACCAAACC	ATATCGCCGG
msa31161.2{327dnt_H36B}	TCGTTTTCAA	TTATTGGATT	CCAATGGACA	CTACCAAACC	ATATCGCCGG
Consensus	*****	*****	*****	*****	*****
	401				450
msa31161.2{327dnt_2603}	ATTCACCTCT	ACAAAAGAGT	AGGGGAGCTA	ATTGGGTCAA	TGTGTATCGT
msa31161.2{327d_18RS21}	ATTCACCTCT	ACAAAAGAGT	AGGGGAGCTA	ATTGGGTCAA	TGTGTATCGT
msa31161.2{327dnt_H36B}	ATTCACCTCT	ACAAAAGAGT	AGGGGAGCTA	ATTGGGTCAA	TGTGTATCGT
Consensus	*****	*****	*****	*****	*****
	451				500
msa31161.2{327dnt_2603}	GTGGCTAATA	ATTTAGCGGA	TCGTATTAGT	CGAGATATTG	AACAGTTTCT
msa31161.2{327d_18RS21}	GTGGCTAATA	ATTTAGCGGA	TCGTATTAGT	CGAGATATTG	AACAGTTTCT
msa31161.2{327dnt_H36B}	GTGGCTAATA	ATTTAGCGGA	TCGTATTAGT	CGAGATATTG	AACAGTTTCT
Consensus	*****	*****	*****	*****	*****
	501				550
msa31161.2{327dnt_2603}	CTTAACCTAC	GAGCCTGAGC	TTGAAACTAG	AGCTGATGAA	ACTGTTCTAG
msa31161.2{327d_18RS21}	CTTAACCTAC	GAGCCTGAGC	TTGAAACTAG	AGCTGATGAA	ACTGTTCTAG
msa31161.2{327dnt_H36B}	CTTAACCTAC	GAGCCTGAGC	TTGAAACTAG	AGCTGATGAA	ACTGTTCTAG
Consensus	*****	*****	*****	*****	*****
	551				600
msa31161.2{327dnt_2603}	AAAATGAAGA	AACTGTTGAT	GAGCACAAAA	CAAGTGTTC	TCAAGCAATA
msa31161.2{327d_18RS21}	AAAATGAAGA	AACTGTTGAT	GAGCACAAAA	CAAGTGTTC	TCAAGCAATA
msa31161.2{327dnt_H36B}	AAAATGAAGA	AACTGTTGAT	GAGCACAAAA	CAAGTGTTC	TCAAGCAATA
Consensus	*****	*****	*****	*****	*****
	601				650
msa31161.2{327dnt_2603}	TCITTTTCGAG	AAGAGGGCTC	TCITGGTTATT	GCTAGTTTGG	ATGTAGATT
msa31161.2{327d_18RS21}	TCITTTTCGAG	AAGAGGGCTC	TCITGGTTATT	GCTAGTTTGG	ATGTAGATT
msa31161.2{327dnt_H36B}	TCITTTTCGAG	AAGAGGGCTC	TCITGGTTATT	GCTAGTTTGG	ATGTAGATT
Consensus	*****	*****	*****	*****	*****
	651				700
msa31161.2{327dnt_2603}	GTCTCAACTA	GATGTTCAAA	TAGGAAAAAC	CAGTCATCTG	CCAGCTTATG
msa31161.2{327d_18RS21}	GTCTCAACTA	GATGTTCAAA	TAGGAAAAAC	CAGTCATCTG	CCAGCTTATG
msa31161.2{327dnt_H36B}	GTCTCAACTA	GATGTTCAAA	TAGGAAAAAC	CAGTCATCTG	CCAGCTTATG
Consensus	*****	*****	*****	*****	*****

Table 70: Comparative Sequences relating to SAG 1280

msa31161.2{327dNt_2603}	701	AAGAGTTATC	CTTACGACGT	AAATTTGAGA	TTCTAACATA	TTTTGACCAA
		AAGAGTTATC	CTTACGACGT	AAATTTGAGA	TTCTAACATA	TTTTGACCAA
		AAGAGTTATC	CTTACGACGT	AAATTTGAGA	TTCTAACATA	TTTTGACCAA
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	751	ATTTCGAAATG	AACGTTCCAA	AGTCCCAAGT	TTTAGACGAG	GTGATTTTGA
		ATTTCGAAATG	AACGTTCCAA	AGTCCCAAGT	TTTAGACGAG	GTGATTTTGA
		ATTTCGAAATG	AACGTTCCAA	AGTCCCAAGT	TTTAGACGAG	GTGATTTTGA
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	801	CACAGAGATG	GAAATGACAC	CAGTCTTTGA	TGGCGAGGAA	TTACTTACTT
		CACAGAGATG	GAAATGACAC	CAGTCTTTGA	TGGCGAGGAA	TTACTTACTT
		CACAGAGATG	GAAATGACAC	CAGTCTTTGA	TGGCGAGGAA	TTACTTACTT
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	851	ATCTCGAAGC	TGATGGCAGT	CCCTATGAGC	TGAAACGAAC	GCTGACTACA
		ATCTCGAAGC	TGATGGCAGT	CCCTATGAGC	TGAAACGAAC	GCTGACTACA
		ATCTCGAAGC	TGATGGCAGT	CCCTATGAGC	TGAAACGAAC	GCTGACTACA
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	901	GTCGAAGAAA	AGGAATTAGA	AAAAATTGGA	CAAGCCATTA	GGATAGAAAA
		GTCGAAGAAA	AGGAATTAGA	AAAAATTGGA	CAAGCCATTA	GGATAGAAAA
		GTCGAAGAAA	AGGAATTAGA	AAAAATTGGA	CAAGCCATTA	GGATAGAAAA
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	951	TCAAGAAAAA	TTGACTCAGC	TAAGGATTGa	TTTATCTCAG	TTTGACCCAG
		TCAAGAAAAA	TTGACTCAGC	TAAGGATTGa	TTTATCTCAG	TTTGACCCAG
		TCAAGAAAAA	TTGACTCAGC	TAAGGATTGr	TTTATCTCAG	TTTGACCCAG
	Consensus	*****	*****	**_*-****-	*****	*****
msa31161.2{327dNt_2603}	1001	ACCGAGTCGG	TATTTTATTG	gATGCAGCAG	GTCGTtTTCG	TTTAaAaAAT
		ACCGAGTCGG	TATTTTATTG	gATGCAGCAG	GTCGTtTTCG	TTTAaAaAAT
		ACCGAGTCGG	TATTTTATTG	kATGCAGCAG	GTCGTyyTCG	TTTAwAwAAT
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	1051	GCAGACCTTG	CTTtACTAGG	TGGTTATCCC	AAAGCCTCGG	TAACtCAACT
		GCAGACCTTG	CTTtACTAGG	TGGTTATCCC	AAAGCCTCGG	TAACtCAACT
		GCAGACCTTG	CTTtACTAGG	TGGTTATCCC	AAAGCCTCGG	TAACtCAACT
	Consensus	*****	***_*-*****	*****	*****	*****
msa31161.2{327dNt_2603}	1101	AGCCCTTGCG	ACAGAActAC	TCCAAATGGG	ACTAAGTCAT	GAAAAGGTTG
		AGCCCTTGCG	ACAGAActAC	TCCAAATGGG	ACTAAGTCAT	GAAAAGGTTG
		AGCCCTTGCG	ACAGAActAC	TCCAAATGGG	ACTAAGTCAT	GAAAAGGTTG
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	1151	AAATTTTCTT	TGGTAGCCAG	CTTCCATTG	AAGAGCTGCG	ACAAGTTGCC
		AAATTTTCTT	TGGTAGCCAG	CTTCCATTG	AAGAGCTGCG	ACAAGTTGCC
		AAATTTTCTT	TGGTAGCCAG	CTTCCATTG	AAGAGCTGCG	ACAAGTTGCC
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	1201	TACGCCTTTT	TatACCAAGA	ACTCAGCAGA	GAAGATGCGG	AGCAATTTGA
		TACGCCTTTT	TacACCAAGA	ACTCAGCAGA	GAAGATGCGG	AGCAATTTGA
		TACGCCTTTT	TacACCAAGA	ACTCAGCAGA	GAAGATGCGG	AGCAATTTGA
	Consensus	*****	**_*-*****	*****	*****	*****
msa31161.2{327dNt_2603}	1251	AAAAGATAAA	GGTAATCAGC	CAGATTTAAC	TCTCAGAGAT	TGGAAAAGCA
		AAAAGATAAA	GGTAATCAGC	CAGATTTAAC	TCTCAGAGAT	TGGAAAAGCA
		AAAAGATAAA	GGTAATCAGC	CAGATTTAAC	TCTCAGAGAT	TGGAAAAGCA
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	1301	AGCTAGAGAA	AGCTGAGGGA	AAAGAAGTAG	TTGATGAAGA	ATTTCGCGAA
		AGCTAGAGAA	AGCTGAGGGA	AAAGAAGTAG	TTGATGAAGA	ATTTCGCGAA
		AGCTAGAGAA	AGCTGAGGGA	AAAGAAGTAG	TTGATGAAGA	ATTTCGCGAA
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	1351	AATCCACTGG	TTCAGAGAGT	ATTGGACACT	TATCCTCTGG	GGTCATTTGGT
		AATCCACTGG	TTCAGAGAGT	ATTGGACACT	TATCCTCTGG	GGTCATTTGGT
		AATCCACTGG	TTCAGAGAGT	ATTGGACACT	TATCCTCTGG	GGTCATTTGGT
	Consensus	*****	*****	*****	*****	*****

Table 70: Comparative Sequences relating to SAG 1280

msa31161.2{327dNt_2603}	1401	TTCTTATAAG	GGACAGGACT	TTGAGGTCAT	GTCGGTCAGC	GATGCTCGAT
		TTCTTATAAG	GGACAGGACT	TTGAGGTCAT	GTCGGTCAGC	GATGCTCGAT
	msa31161.2{327d_18RS21}	TTCTTATAAG	GGACAGGACT	TTGAGGTCAT	GTCGGTCAGC	GATGCTCGAT
	msa31161.2{327dNT_H36B}	TTCTTATAAG	GGACAGGACT	TTGAGGTCAT	GTCGGTCAGC	GATGCTCGAT
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	1451	TGAACGGTTT	GATTTCGGATT	GAGTTAGTCA	ATGACTTTTC	GGATATCATT
		TGAACGGTTT	GATTTCGGATT	GAGTTAGTCA	ATGACTTTTC	GGATATCATT
	msa31161.2{327d_18RS21}	TGAACGGTTT	GATTTCGGATT	GAGTTAGTCA	ATGACTTTTC	GGATATCATT
	msa31161.2{327dNT_H36B}	TGAACGGTTT	GATTTCGGATT	GAGTTAGTCA	ATGACTTTTC	GGATATCATT
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	1501	GAACAAAATC	CAGTTCCTTA	TGTGAGGACC	TGGGAAGAAG	TCAGTCAGGC
		GAACAAAATC	CAGTTCCTTA	TGTGAGGACC	TGGGAAGAAG	TCAGTCAGGC
	msa31161.2{327d_18RS21}	GAACAAAATC	CAGTTCCTTA	TGTGAGGACC	TGGGAAGAAG	TCAGTCAGGC
	msa31161.2{327dNT_H36B}	GAACAAAATC	CAGTTCCTTA	TGTGAGGACC	TGGGAAGAAG	TCAGTCAGGC
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	1551	ACTTCATCAG	CCAAAGGCAG	AACCACAAAC	AGAGTTAGAA	GAAGCGGACC
		ACTTCATCAG	CCAAAGGCAG	AACCACAAAC	AGAGTTAGAA	GAAGCGGACC
	msa31161.2{327d_18RS21}	ACTTCATCAG	CCAAAGGCAG	AACCACAAAC	AGAGTTAGAA	GAAGCGGACC
	msa31161.2{327dNT_H36B}	ACTTCATCAG	CCAAAGGCAG	AACCACAAAC	AGAGTTAGAA	GAAGCGGACC
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	1601	AAGAAATAAA	CCTATTCTCA	TTTCTGGAAG	AGGAGCAGT	TCAGAGTATT
		AAGAAATAAA	CCTATTCTCA	TTTCTGGAAG	AGGAGCAGT	TCAGAGTATT
	msa31161.2{327d_18RS21}	AAGAAATAAA	CCTATTCTCA	TTTCTGGAAG	AGGAGCAGT	TCAGAGTATT
	msa31161.2{327dNT_H36B}	AAGAAATAAA	CCTATTCTCA	TTTCTGGAAG	AGGAGCAGT	TCAGAGTATT
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	1651	GGACTATTGG	AACCAGATGA	TTCAGAAAAT	GGTCATAACG	ATACTGATCT
		GGACTATTGG	AACCAGATGA	TTCAGAAAAT	GGTCATAACG	ATACTGATCT
	msa31161.2{327d_18RS21}	GGACTATTGG	AACCAGATGA	TTCAGAAAAT	GGTCATAACG	ATACTGATCT
	msa31161.2{327dNT_H36B}	GGACTATTGG	AACCAGATGA	TTCAGAAAAT	GGTCATAACG	ATACTGATCT
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	1701	TGAAGAAACA	GATAATCAAA	TTCTGAAGA	GGAAGTCGTC	GAAACAATTC
		TGAAGAAACA	GATAATCAAA	TTCTGAAGA	GGAAGTCGTC	GAAACAATTC
	msa31161.2{327d_18RS21}	TGAAGAAACA	GATAATCAAA	TTCTGAAGA	GGAAGTCGTC	GAAACAATTC
	msa31161.2{327dNT_H36B}	TGAAGAAACA	GATAATCAAA	TTCTGAAGA	GGAAGTCGTC	GAAACAATTC
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	1751	CAGAGATTCC	AGTAACGGAC	TTTTATTTTC	CAGAAGATTT	GACGGACTTT
		CAGAGATTCC	AGTAACGGAC	TTTTATTTTC	CAGAAGATTT	GACGGACTTT
	msa31161.2{327d_18RS21}	CAGAGATTCC	AGTAACGGAC	TTTTATTTTC	CAGAAGATTT	GACGGACTTT
	msa31161.2{327dNT_H36B}	CAGAGATTCC	AGTAACGGAC	TTTTATTTTC	CAGAAGATTT	GACGGACTTT
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	1801	TATCCTAAGA	CTGCTAGAGA	TAAGGTTGAG	ACAAACATTG	TGGCCATTTC
		TATCCTAAGA	CTGCTAGAGA	TAAGGTTGAG	ACAAACATTG	TGGCCATTTC
	msa31161.2{327d_18RS21}	TATCCTAAGA	CTGCTAGAGA	TAAGGTTGAG	ACAAACATTG	TGGCCATTTC
	msa31161.2{327dNT_H36B}	TATCCTAAGA	CTGCTAGAGA	TAAGGTTGAG	ACAAACATTG	TGGCCATTTC
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	1851	TTTGGTAAAA	AATCTAGAAG	TAGAGCACCG	CAATGCTTCA	CCAAGTGAAC
		TTTGGTAAAA	AATCTAGAAG	TAGAGCACCG	CAATGCTTCA	CCAAGTGAAC
	msa31161.2{327d_18RS21}	TTTGGTAAAA	AATCTAGAAG	TAGAGCACCG	CAATGCTTCA	CCAAGTGAAC
	msa31161.2{327dNT_H36B}	TTTGGTAAAA	AATCTAGAAG	TAGAGCACCG	CAATGCTTCA	CCAAGTGAAC
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	1901	AAGAACTCCT	TGCCAAGTAT	GTAGGCTGGG	GTGGACTAGC	CAATGAATTT
		AAGAACTCCT	TGCCAAGTAT	GTAGGCTGGG	GTGGACTAGC	CAATGAATTT
	msa31161.2{327d_18RS21}	AAGAACTCCT	TGCCAAGTAT	GTAGGCTGGG	GTGGACTAGC	CAATGAATTT
	msa31161.2{327dNT_H36B}	AAGAACTCCT	TGCCAAGTAT	GTAGGCTGGG	GTGGACTAGC	CAATGAATTT
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	1951	TTTGATGACT	ATAATCCAAA	ATTTTCTAAG	GAACGAGAAG	AACTGAAGAG
		TTTGATGACT	ATAATCCAAA	ATTTTCTAAG	GAACGAGAAG	AACTGAAGAG
	msa31161.2{327d_18RS21}	TTTGATGACT	ATAATCCAAA	ATTTTCTAAG	GAACGAGAAG	AACTGAAGAG
	msa31161.2{327dNT_H36B}	TTTGATGACT	ATAATCCAAA	ATTTTCTAAG	GAACGAGAAG	AACTGAAGAG
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2001	CCTAGTCACA	GATAAAGAGT	ATTCGGATAT	GAAACAGTCC	TCCCTGACAG
		CCTAGTCACA	GATAAAGAGT	ATTCGGATAT	GAAACAGTCC	TCCCTGACAG
	msa31161.2{327d_18RS21}	CCTAGTCACA	GATAAAGAGT	ATTCGGATAT	GAAACAGTCC	TCCCTGACAG
	msa31161.2{327dNT_H36B}	CCTAGTCACA	GATAAAGAGT	ATTCGGATAT	GAAACAGTCC	TCCCTGACAG
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2051	CCTATTACAC	AGACCCATCC	CTGATCCGTC	AGATGTGGGA	TAAGTTGGAA
		CCTATTACAC	AGACCCATCC	CTGATCCGTC	AGATGTGGGA	TAAGTTGGAA
	msa31161.2{327d_18RS21}	CCTATTACAC	AGACCCATCC	CTGATCCGTC	AGATGTGGGA	TAAGTTGGAA
	msa31161.2{327dNT_H36B}	CCTATTACAC	AGACCCATCC	CTGATCCGTC	AGATGTGGGA	TAAGTTGGAA

Table 70: Comparative Sequences relating to SAG 1280

Consensus	*****	*****	*****	*****	*****
	2101				2150
msa31161.2{327dNt_2603}	AGAGATGGCT	TTACAGGTGG	CAAAATCCTA	GATCCTTCCA	TGGGAACAGG
msa31161.2{327d_18RS21}	AGAGATGGCT	TTACAGGTGG	CAAAATCCTA	GATCCTTCCA	TGGGAACAGG
msa31161.2{327dNT_H36B}	AGAGATGGCT	TTACAGGTGG	CAAAATCCTA	GATCCTTCCA	TGGGAACAGG
Consensus	*****	*****	*****	*****	*****
	2151				2200
msa31161.2{327dNt_2603}	GAATTTCTTT	GCGGCTATGC	CAAAACACTT	AAGAGAAAAG	AGTGAGTTGT
msa31161.2{327d_18RS21}	GAATTTCTTT	GCGGCTATGC	CAAAACACTT	AAGAGAAAAG	AGTGAGTTGT
msa31161.2{327dNT_H36B}	GAATTTCTTT	GCGGCTATGC	CAAAACACTT	AAGAGAAAAG	AGTGAGTTGT
Consensus	*****	*****	*****	*****	*****
	2201				2250
msa31161.2{327dNt_2603}	ATGGCGTAGA	GTTAGATACT	ATTACAGGAG	CTATTGCCAA	ACACCTTCAT
msa31161.2{327d_18RS21}	ATGGCGTAGA	GTTAGATACT	ATTACAGGAG	CTATTGCCAA	ACACCTTCAT
msa31161.2{327dNT_H36B}	ATGGCGTAGA	GTTAGATACT	ATTACAGGAG	CTATTGCCAA	ACACCTTCAT
Consensus	*****	*****	*****	*****	*****
	2251				2300
msa31161.2{327dNt_2603}	CCCAATAGTC	ATATTGAAAT	TAAGGGATTT	GAGACGGTGG	CTTTTAACGA
msa31161.2{327d_18RS21}	CCCAATAGTC	ATATTGAAAT	TAAGGGATTT	GAGACGGTGG	CTTTTAACGA
msa31161.2{327dNT_H36B}	CCCAATAGTC	ATATTGAAAT	TAAGGGATTT	GAGACGGTGG	CTTTTAACGA
Consensus	*****	*****	*****	*****	*****
	2301				2350
msa31161.2{327dNt_2603}	CAATAGTTTT	GATTTGGTGA	TTTCAAATGT	GCCCTTTGCC	AATATACGAA
msa31161.2{327d_18RS21}	CAATAGTTTT	GATTTGGTGA	TTTCAAATGT	GCCCTTTGCC	AATATACGAA
msa31161.2{327dNT_H36B}	CAATAGTTTT	GATTTGGTGA	TTTCAAATGT	GCCCTTTGCC	AATATACGAA
Consensus	*****	*****	*****	*****	*****
	2351				2400
msa31161.2{327dNt_2603}	TTGCGGATAA	TAGGTACGAT	AGGCCTTACA	TGATTCATGA	CTACTTTGTC
msa31161.2{327d_18RS21}	TTGCGGATAA	TAGGTACGAT	AGGCCTTACA	TGATTCATGA	CTACTTTGTC
msa31161.2{327dNT_H36B}	TTGCGGATAA	TAGGTACGAT	AGGCCTTACA	TGATTCATGA	CTACTTTGTC
Consensus	*****	*****	*****	*****	*****
	2401				2450
msa31161.2{327dNt_2603}	AAAAAGTCAC	TTGATTGCT	TCATGATGGT	GGACAAGTAG	CGATTATCTC
msa31161.2{327d_18RS21}	AAAAAGTCAC	TTGATTGCT	TCATGATGGT	GGACAAGTAG	CGATTATCTC
msa31161.2{327dNT_H36B}	AAAAAGTCAC	TTGATTGCT	TCATGATGGT	GGACAAGTAG	CGATTATCTC
Consensus	*****	*****	*****	*****	*****
	2451				2500
msa31161.2{327dNt_2603}	TTCCACAGGA	ACTATGGATA	AGCGAACAGA	AAACATCTTA	CAAGATATTC
msa31161.2{327d_18RS21}	TTCCACAGGA	ACTATGGATA	AGCGAACAGA	AAACATCTTA	CAAGATATTC
msa31161.2{327dNT_H36B}	TTCCACAGGA	ACTATGGATA	AGCGAACAGA	AAACATCTTA	CAAGATATTC
Consensus	*****	*****	*****	*****	*****
	2501				2550
msa31161.2{327dNt_2603}	GTGAGACAAC	TGAATTTCTT	GGTGGGGTTC	GACTGCCTGA	CTCTGCCTTT
msa31161.2{327d_18RS21}	GTGAGACAAC	TGAATTTCTT	GGTGGGGTTC	GACTGCCTGA	CTCTGCCTTT
msa31161.2{327dNT_H36B}	GTGAGACAAC	TGAATTTCTT	GGTGGGGTTC	GACTGCCTGA	CTCTGCCTTT
Consensus	*****	*****	*****	*****	*****
	2551				2600
msa31161.2{327dNt_2603}	AAGGCCATTG	CAGGAACGAG	TGTCACAACG	GATATGTTAT	TCITCCAGAA
msa31161.2{327d_18RS21}	AAGGCCATTG	CAGGAACGAG	TGTCACAACG	GATATGTTAT	TCITCCAGAA
msa31161.2{327dNT_H36B}	AAGGCCATTG	CAGGAACGAG	TGTCACAACG	GATATGTTAT	TCITCCAGAA
Consensus	*****	*****	*****	*****	*****
	2601				2650
msa31161.2{327dNt_2603}	ACACTTAGAC	AAGGGATATG	TGGCAGACGA	TTTAGCCTTT	TCAGGTTCCA
msa31161.2{327d_18RS21}	ACACTTAGAC	AAGGGATATG	TGGCAGACGA	TTTAGCCTTT	TCAGGTTCCA
msa31161.2{327dNT_H36B}	ACACTTAGAC	AAGGGATATG	TGGCAGACGA	TTTAGCCTTT	TCAGGTTCCA
Consensus	*****	*****	*****	*****	*****
	2651				2700
msa31161.2{327dNt_2603}	TTTCGCTATGA	CAAGGATAGT	CGCATTTGGC	TCAATCCTTA	TTTTGATGGA
msa31161.2{327d_18RS21}	TTTCGCTATGA	CAAGGATAGT	CGCATTTGGC	TCAATCCTTA	TTTTGATGGA
msa31161.2{327dNT_H36B}	TTTCGCTATGA	CAAGGATAGT	CGCATTTGGC	TCAATCCTTA	TTTTGATGGA
Consensus	*****	*****	*****	*****	*****
	2701				2750
msa31161.2{327dNt_2603}	GAATACAATA	GCCAGGTGCT	AGGAACCTAC	GAGGTCAGGA	ATTTTAACGG
msa31161.2{327d_18RS21}	GAATACAATA	GCCAGGTGCT	AGGAACCTAC	GAGGTCAGGA	ATTTTAACGG
msa31161.2{327dNT_H36B}	GAATACAATA	GCCAGGTGCT	AGGAACCTAC	GAGGTCAGGA	ATTTTAACGG
Consensus	*****	*****	*****	*****	*****
	2751				2800
msa31161.2{327dNt_2603}	AGGAACACTT	TCTGTTAAGG	GGACTAGTGA	TGACTTGATT	GCAAGTGTG
msa31161.2{327d_18RS21}	AGGAACACTT	TCTGTTAAGG	GGACTAGTGA	TGACTTGATT	GCAAGTGTG

Table 70: Comparative Sequences relating to SAG 1280

msa31161.2{327dnt_H36B}	AGGAACACTT	TCTGTTAAGG	GGACTAGTGA	TGACTTGATT	GCAAGTGTG
Consensus	*****	*****	*****	*****	*****
	2801				2850
msa31161.2{327dnt_2603}	AAACAGCTCT	AAATCACGTT	AAGGCCCAA	GAGAGATTGA	TAGAAATGAG
msa31161.2{327d_18RS21}	AAACAGCTCT	AAATCACGTT	AAGGCCCAA	GAGAGATTGA	TAGAAATGAG
msa31161.2{327dnt_H36B}	AAACAGCTCT	AAATCACGTT	AAGGCCCAA	GAGAGATTGA	TAGAAATGAG
Consensus	*****	*****	*****	*****	*****
	2851				2900
msa31161.2{327dnt_2603}	GTCATCATT	ACCCAGATGT	GTTGACCAA	CAAGTCAATG	ATACCTCCAT
msa31161.2{327d_18RS21}	GTCATCATT	ACCCAGATGT	GTTGACCAA	CAAGTCAATG	ATACCTCCAT
msa31161.2{327dnt_H36B}	GTCATCATT	ACCCAGATGT	GTTGACCAA	CAAGTCAATG	ATACCTCCAT
Consensus	*****	*****	*****	*****	*****
	2901				2950
msa31161.2{327dnt_2603}	TCCAGCTGAA	ATGAGGGAAA	ATCTAGGTCA	GTACAGTTT	GGTTATCAGG
msa31161.2{327d_18RS21}	TCCAGCTGAA	ATGAGGGAAA	ATCTAGGTCA	GTACAGTTT	GGTTATCAGG
msa31161.2{327dnt_H36B}	TCCAGCTGAA	ATGAGGGAAA	ATCTAGGTCA	GTACAGTTT	GGTTATCAGG
Consensus	*****	*****	*****	*****	*****
	2951				3000
msa31161.2{327dnt_2603}	GGTCTACAGT	TTACTATCGA	GATAACAAAG	GCATTTCGAGT	CGGAACCAAG
msa31161.2{327d_18RS21}	GGTCTACAGT	TTACTATCGA	GATAACAAAG	GCATTTCGAGT	CGGAACCAAG
msa31161.2{327dnt_H36B}	GGTCTACAGT	TTACTATCGA	GATAACAAAG	GCATTTCGAGT	CGGAACCAAG
Consensus	*****	*****	*****	*****	*****
	3001				3033
msa31161.2{327dnt_2603}	ACGGAAGAAA	TCAGTTACTA	TGTCGATGAA	GAG	
msa31161.2{327d_18RS21}	ACGGAAGAAA	TCAGTTACTA	TGTCGATGAA	GAG	
msa31161.2{327dnt_H36B}	ACGGAAGAAA	TCAGTTACTA	TGTCGATGAA	GAG	
Consensus	*****	*****	*****	***	

SEQ ID. NO. 7004

STRAIN H36B frame: 1

GGKMNQEVLLQMMRATIPDRALLEAFLLYQAEHFDEWDLSLIHQFMTNRQEIINKSVQVL
HFETDVSAFVQASPYDTAHDLLTYTQVFGQSGLQKLDKLSPEKNLVIEVALFNLATRFQ
LLDSNGHYQTISPDSLLQKSRGANLVNVYRVANNLADRISRDIEQFLTYEPELETRADE
TVLENEETVDEHKTSTVHQAI SFREEGSLVIA SLDVDLSQLDVQIGKTSHPAYEELSRLR
KFEILTYFDQIRNERSKVPSFRRGDFDTEMEMTPVFDGEEELLTYLEADGSPYELKRTLT
VEEKELEKIGQAIRIENQEKLTQLXIXLSQFDPDRVGILLXAGRXRLKNADLASLGYP
KASVTQLALATELLQMLSHKVEFFFGSLSIEELRQVAYAFLLHQELSREDAEQFEKDK
GNQPDLTLRDWKSKLEKAEKGVVDEEFAENPLVQVRVLDITYPLGSLVSYKGQDFEVM SVS
DARLNGLRIRIELVNDFSDI IEQNPVLYVRTWEEVSQALHQPKAEPQTELEADQELNLF
FLEELVQSIGLLEPDDSENGHNDTLEETDNIPEEEVETIPEIPVTDIFYFPEDLTDF
YPKTARDKVETNI VAI RLKVNLEVEHRNASPSEQELLAKYVGWGLANEFFDDYNPKFSK
EREELKSLVTDKEYSDMKQSSLTAYYTDPSLIRQMWDKLERDGTGGKILDPSMG TG NFF
AAMPKHLREKSELYGVELDTITGAI AKHLHPNSHIEIKGFETVAFNDNSFDLVI SNVPFA
NIRIADNRYDRPYMIHDYFVKKSLDLLHDGGQVAI ISSTGTMDKRTENILQDIRETTEFL
GGVRLPDSAFKAIAGTSVTTDMLFFQKHLKGYVADDLAFSGSIRYDKDSRIWLNPFYFDG
EYNSQVLGTYEVRNFGGTL SVKGTSDDLIASVETALNHVKAPREIDRNEVI INPDVLTK
QVNDTSIPAEMRENLGQYSFGYQGSTVYVRDNGKIRVGTKTEEISYYVDEE

SEQ ID. NO. 7005

STRAIN 18RS21 frame: 1

XGKMNQEVLLQMMRATIPDRALLEAFLLYQAEHFDEWDLSLIHQFMTNRQEIINKSVQVL
HFETDVSAFVQASPYDTAHDLLTYTQVFGQSGLQKLDKLSPEKNLVIEVALFNLATRFQ
LLDSNGHYQTISPDSLLQKSRGANLVNVYRVANNLADRISRDIEQFLTYEPELETRADE
TVLENEETVDEHKTSTVHQAI SFREEGSLVIA SLDVDLSQLDVQIGKTSHPAYEELSRLR
KFEILTYFDQIRNERSKVPSFRRGDFDTEMEMTPVFDGEEELLTYLEADGSPYELKRTLT
VEEKELEKIGQAIRIENQEKLTQLGIDLSQFDPDRVGILLDAAGFRFLKNADLALLGGYP
KASVTQLALATELLQMLSHKVEFFFGSLSIEELRQVAYAFLLHQELSREDAEQFEKDK
GNQPDLTLRDWKSKLEKAEKGVVDEEFAENPLVQVRVLDITYPLGSLVSYKGQDFEVM SVS
DARLNGLRIRIELVNDFSDI IEQNPVLYVRTWEEVSQALHQPKAEPQTELEADQELNLF
FLEELVQSIGLLEPDDSENGHNDTLEETDNIPEEEVETIPEIPVTDIFYFPEDLTDF
YPKTARDKVETNI VAI RLKVNLEVEHRNASPSEQELLAKYVGWGLANEFFDDYNPKFSK
EREELKSLVTDKEYSDMKQSSLTAYYTDPSLIRQMWDKLERDGTGGKILDPSMG TG NFF
AAMPKHLREKSELYGVELDTITGAI AKHLHPNSHIEIKGFETVAFNDNSFDLVI SNVPFA
NIRIADNRYDRPYMIHDYFVKKSLDLLHDGGQVAI ISSTGTMDKRTENILQDIRETTEFL
GGVRLPDSAFKAIAGTSVTTDMLFFQKHLKGYVADDLAFSGSIRYDKDSRIWLNPFYFDG
EYNSQVLGTYEVRNFGGTL SVKGTSDDLIASVETALNHVKAPREIDRNEVI INPDVLTK
QVNDTSIPAEMRENLGQYSFGYQGSTVYVRDNGKIRVGTKTEEISYYVDEE

SEQ ID. NO. 7006

STRAIN 2603 frame: 1

GGKMNQEVLLQMMRATIPDRALLEAFLLYQAEHFDEWDLSLIHQFMTNRQEIINKSVQVL
HFETDVSAFVQASPYDTAHDLLTYTQVFGQSGLQKLDKLSPEKNLVIEVALFNLATRFQ
LLDSNGHYQTISPDSLLQKSRGANLVNVYRVANNLADRISRDIEQFLTYEPELETRADE
TVLENEETVDEHKTSTVHQAI SFREEGSLVIA SLDVDLSQLDVQIGKTSHPAYEELSRLR
KFEILTYFDQIRNERSKVPSFRRGDFDTEMEMTPVFDGEEELLTYLEADGSPYELKRTLT
VEEKELEKIGQAIRIENQEKLTQLGIDLSQFDPDRVGILLDAAGFRFLKNADLALLGGYP
KASVTQLALATELLQMLSHKVEFFFGSLSIEELRQVAYAFLLHQELSREDAEQFEKDK
GNQPDLTLRDWKSKLEKAEKGVVDEEFAENPLVQVRVLDITYPLGSLVSYKGQDFEVM SVS

Table 70: Comparative Sequences relating to SAG 1280

DARLNGLIRIELVNDFSDIIEQNPVLYVRTWEEVSQALHQPKEPQTELEBDAQELNLFSS
 FLEEEpVQSIGLLEPDDSENGHNDTDLEETDNQIPEEEVETIPEIPVTDFFPEDLTDF
 YPKTARDKVTNIVAIRLVNLEVEHRNASPEQELLAKYVGWGGLANEFFDDYNPKFSK
 EREELKSLVTDKEYSDMKQSSLTAYYTDPSLRIRQMWKLERDGTGGKILDPMSGTGNFF
 AAMPKHLREKSELYGVELDTITGAIKHLHPNSHIEIKGFETVAFNDNSFDLVISNVFFA
 NIRIADNRYDRPYMIHDYFVKSLDLLHDGGQVAIISSTGTMDKRTENILQDIRETTEFL
 GGVRLPDSAFKAIAGTSVTMDMLFFQKHLDKGYVADDLAFSGSIRYDKDSRIWLNPFYDG
 EYNSQVLGTYEVRNFGGTLVSVKGTSDDLIASVETALNHVKAPREIDRNEVINPDLVTK
 QVNDTSIPAEEMRENLGQYSPGYQGSTVYIRDNGKIRVGTKEEISYYVDEE

PRETTY of: /biotmp/msa23816.2{*} June 20, 2002 11:04 ..

msa23816.2{327dnt_H36B}	1	50
msa23816.2{327dnt_2603}	gGKMNQEVLL QMMRATIPRD RALLEAFLLY QAEEHFDEEWD SLIHQFMNTR	
msa23816.2{327d_18RS21}	gGKMNQEVLL QMMRATIPRD RALLEAFLLY QAEEHFDEEWD SLIHQFMNTR	
Consensus	-*****	
msa23816.2{327dnt_H36B}	51	100
msa23816.2{327dnt_2603}	QEINKSVQVL HFETDVSAFV QASPYDTAHD LLTYTQVFGQ SGLQKLDKLS	
msa23816.2{327d_18RS21}	QEINKSVQVL HFETDVSAFV QASPYDTAHD LLTYTQVFGQ SGLQKLDKLS	
Consensus	*****	
msa23816.2{327dnt_H36B}	101	150
msa23816.2{327dnt_2603}	PSEKNLVIEV ALFNLATRFQ LLDSNGHYQT ISPDSLLQKS RANLVNVYR	
msa23816.2{327d_18RS21}	PSEKNLVIEV ALFNLATRFQ LLDSNGHYQT ISPDSLLQKS RANLVNVYR	
Consensus	*****	
msa23816.2{327dnt_H36B}	151	200
msa23816.2{327dnt_2603}	VANNLADRIS RDIEQFLITY EPELETRADE TVLENEETVD EHKTSVHQAI	
msa23816.2{327d_18RS21}	VANNLADRIS RDIEQFLITY EPELETRADE TVLENEETVD EHKTSVHQAI	
Consensus	*****	
msa23816.2{327dnt_H36B}	201	250
msa23816.2{327dnt_2603}	SFREGSLVI ASLDVDLSQL DVQIGKTSHL PAYEELSLRR KFEILTYFDQ	
msa23816.2{327d_18RS21}	SFREGSLVI ASLDVDLSQL DVQIGKTSHL PAYEELSLRR KFEILTYFDQ	
Consensus	*****	
msa23816.2{327dnt_H36B}	251	300
msa23816.2{327dnt_2603}	IRNERSKVPS FRRGDFDTEM EMTFVFDGEE LLTYLEADGS PYELKRTLIT	
msa23816.2{327d_18RS21}	IRNERSKVPS FRRGDFDTEM EMTFVFDGEE LLTYLEADGS PYELKRTLIT	
Consensus	*****	
msa23816.2{327dnt_H36B}	301	350
msa23816.2{327dnt_2603}	VEEKELEKIG QAIRIENQEK LTQLxIxLSQ FDPDRVIGILL xAAGRrRLxN	
msa23816.2{327d_18RS21}	VEEKELEKIG QAIRIENQEK LTQLgIdLSQ FDPDRVIGILL dAAGRrRLkN	
Consensus	*****	
msa23816.2{327dnt_H36B}	351	400
msa23816.2{327dnt_2603}	ADLAsLGGYP KASVTQLALA TELLQMGLSH EKVEFFFGSQ LSIEELRQVA	
msa23816.2{327d_18RS21}	ADLAlLGGYP KASVTQLALA TELLQMGLSH EKVEFFFGSQ LSIEELRQVA	
Consensus	****-*****	
msa23816.2{327dnt_H36B}	401	450
msa23816.2{327dnt_2603}	YAFhQELSR EDAAEQFEKDK GNQPDLTlRD WSKLEKAEG KEVVDEEFAB	
msa23816.2{327d_18RS21}	YAFlyQELSR EDAAEQFEKDK GNQPDLTlRD WSKLEKAEG KEVVDEEFAB	
Consensus	****-*****	
msa23816.2{327dnt_H36B}	451	500
msa23816.2{327dnt_2603}	NPLVQRVLDI YPLGSLVSYK QDQFEVMSVS DARLNGLIRI ELVNDFSDI	
msa23816.2{327d_18RS21}	NPLVQRVLDI YPLGSLVSYK QDQFEVMSVS DARLNGLIRI ELVNDFSDI	
Consensus	*****	
msa23816.2{327dnt_H36B}	501	550
msa23816.2{327dnt_2603}	EQNPVLYVRT WEEVSQALHQ PKAEPQTELE EADQELNLFSS FLEEEpVQSI	
msa23816.2{327d_18RS21}	EQNPVLYVRT WEEVSQALHQ PKAEPQTELE EADQELNLFSS FLEEEpVQSI	
Consensus	*****	
msa23816.2{327dnt_H36B}	551	600
msa23816.2{327dnt_2603}	GLLEPDDSEN GHNDTDLEET DNQIPEEEV ETIPEIPVTD FYFPEDLTDF	
msa23816.2{327d_18RS21}	GLLEPDDSEN GHNDTDLEET DNQIPEEEV ETIPEIPVTD FYFPEDLTDF	
Consensus	*****	

Table 70: Comparative Sequences relating to SAG 1280

	601				650
msa23816.2{327dNT_H36B}	YPKTARDKVE	TNIVAIRLVK	NLEVEHRNAS	PSEQELLAKY	VGWGGLANEF
msa23816.2{327dNT_2603}	YPKTARDKVE	TNIVAIRLVK	NLEVEHRNAS	PSEQELLAKY	VGWGGLANEF
msa23816.2{327d_18RS21}	YPKTARDKVE	TNIVAIRLVK	NLEVEHRNAS	PSEQELLAKY	VGWGGLANEF
Consensus	*****	*****	*****	*****	*****
	651				700
msa23816.2{327dNT_H36B}	FDDYNPKFSK	EREELKSLVT	DKEYSDMKQS	SLTAYYTDPS	LIRQMWDKLE
msa23816.2{327dNT_2603}	FDDYNPKFSK	EREELKSLVT	DKEYSDMKQS	SLTAYYTDPS	LIRQMWDKLE
msa23816.2{327d_18RS21}	FDDYNPKFSK	EREELKSLVT	DKEYSDMKQS	SLTAYYTDPS	LIRQMWDKLE
Consensus	*****	*****	*****	*****	*****
	701				750
msa23816.2{327dNT_H36B}	RDGFTGGKIL	DPSMGTGNFF	AAMPKHLREK	SELYGVELDT	ITGAIAKHLH
msa23816.2{327dNT_2603}	RDGFTGGKIL	DPSMGTGNFF	AAMPKHLREK	SELYGVELDT	ITGAIAKHLH
msa23816.2{327d_18RS21}	RDGFTGGKIL	DPSMGTGNFF	AAMPKHLREK	SELYGVELDT	ITGAIAKHLH
Consensus	*****	*****	*****	*****	*****
	751				800
msa23816.2{327dNT_H36B}	PNSHIEIKGF	ETVAFNDNSF	DLVISNVPFA	NIRIADNRYD	RPYMIHDYFV
msa23816.2{327dNT_2603}	PNSHIEIKGF	ETVAFNDNSF	DLVISNVPFA	NIRIADNRYD	RPYMIHDYFV
msa23816.2{327d_18RS21}	PNSHIEIKGF	ETVAFNDNSF	DLVISNVPFA	NIRIADNRYD	RPYMIHDYFV
Consensus	*****	*****	*****	*****	*****
	801				850
msa23816.2{327dNT_H36B}	KKSLDLLHDG	GQVAIISSTG	TMDKRTENIL	QDIRETTEFL	GGVRLPDSAF
msa23816.2{327dNT_2603}	KKSLDLLHDG	GQVAIISSTG	TMDKRTENIL	QDIRETTEFL	GGVRLPDSAF
msa23816.2{327d_18RS21}	KKSLDLLHDG	GQVAIISSTG	TMDKRTENIL	QDIRETTEFL	GGVRLPDSAF
Consensus	*****	*****	*****	*****	*****
	851				900
msa23816.2{327dNT_H36B}	KAIAGTSVTT	DMLFFQKHL	KGYVADDLAF	SGSIRYDKDS	RIWLNPFYFDG
msa23816.2{327dNT_2603}	KAIAGTSVTT	DMLFFQKHL	KGYVADDLAF	SGSIRYDKDS	RIWLNPFYFDG
msa23816.2{327d_18RS21}	KAIAGTSVTT	DMLFFQKHL	KGYVADDLAF	SGSIRYDKDS	RIWLNPFYFDG
Consensus	*****	*****	*****	*****	*****
	901				950
msa23816.2{327dNT_H36B}	EYNSQVLGTY	EVRFNNGGTL	SVKGTSDDLI	ASVETALNHV	KAPREIDRNE
msa23816.2{327dNT_2603}	EYNSQVLGTY	EVRFNNGGTL	SVKGTSDDLI	ASVETALNHV	KAPREIDRNE
msa23816.2{327d_18RS21}	EYNSQVLGTY	EVRFNNGGTL	SVKGTSDDLI	ASVETALNHV	KAPREIDRNE
Consensus	*****	*****	*****	*****	*****
	951				1000
msa23816.2{327dNT_H36B}	VIINPDVLTK	QVNDTSIPAE	MRENLGQYSF	GYQGSTVYYR	DNKGIRVGTK
msa23816.2{327dNT_2603}	VIINPDVLTK	QVNDTSIPAE	MRENLGQYSF	GYQGSTVYYR	DNKGIRVGTK
msa23816.2{327d_18RS21}	VIINPDVLTK	QVNDTSIPAE	MRENLGQYSF	GYQGSTVYYR	DNKGIRVGTK
Consensus	*****	*****	*****	*****	*****
	1001	1011			
msa23816.2{327dNT_H36B}	TEEISYYVDE	E			
msa23816.2{327dNT_2603}	TEEISYYVDE	E			
msa23816.2{327d_18RS21}	TEEISYYVDE	E			
Consensus	*****	*			

Table 71: Comparative Sequences relating to SAG1333

SEQ ID NO. 7101

STRAIN 2603

ATGAAAAAGAAAATTTATTTGAAAAGTAGTGTCTTGGTTTAGTCGCTGGGACTTCTATTT
 ATGTTCTCAAGCGTGTTCGCGGACCAAGTCCGCTGTCCTGATGGAAGTTATAGGCGTCAATGACTTT
 CATGGTGCACCTTGACAATCTGGAACAGCAAAATATGCTGATGGAAGTTGCTAATGCT
 GGTACTGCTGCTCAATTAGATGCTTATATGGATGACGCTCAAAAAGATTTCAAACAACT
 AACCCTAATGGTGAAGCATTAGGGTTCAAGCAGGCGATATGGTTGGAGCAAGTCCAGCC
 AACTCTGGGCTTCTTCAAGATGAACCAACTGTCAAAAATTTTAAATGCAATGAATGTTGAG
 TATGGCACATTGGGTAACCATGAATTTGATGAAGGGTTGGCAGAATATAATCGTATCGTT
 ACTGGTAAAGCCCCGTCTCCAGATTCTAATATTATAATATTACGAAATCATACCCACAT
 GAAGCTGCAAAACAAAGAAATTTAGTGGCAAAATGTTATGATAAAGTTAAACAAACAAAT
 CCTTACAATTGGAAGCCTTACGCTATTAAAAATATTCCTGTAATAACAAAGTGTGAAC
 GTTGGCTTTATCGGGATTGTCAACCAAGACATCCCAACCTTGTCTTACGTAAAAATTTAT
 GAACAATATGAATTTTAGATGAAGCTGAAACAATCGTTAAATACGCCAAAGAAATTACAA
 GCTAAAAATGTCAAAGCTATTGTAGTTCTCGCACATGTACCTGCAACAAGTAAAAATGAT
 ATTGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCTGAAAAAT
 AGCGTAGATATTGTCTTGTCTGGACACAATCATCAATATACAAATGGTCTTGTGGTAAA
 ACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAGCCTATGTGATGTACGTGGTGTCTTA
 GATACTGATACACAAGATTTTATTGAGACCCCTTCAAGTAAAGTAATTGCAGTTGCTCCT
 GGTAAAAAAGCAGGTAGTCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTT
 AAACAAGTAAACAGAAAGCAGCAAAATTTGGTACTGCGAGGTAAAGTGTATGATTACGCGTTCT
 GTTGATCAAGATAATGTTAGTCCGCTAGGCGACCTCATCAGAGGCTCAACTAGCAATT
 GCTCGAAAAAGCTGGCCAGATATCGATTTTGGCATGACAATAATGGTGGCAATTCGTGCT
 GACTTACTCATCAAAACAGATGGAACAATCACTGGGGAGCTGCACAAGCAGTTCAACCT
 TTTGGTAAATATCTTACAAGTCTGCGAAATTAAGTGGTAGAGATCTTTATAAAGCACTCAAC
 GAACAATACGACCAAAACAAATTTCTTCTTCAATAGCTGGTCTGCGATACACTTAC
 ACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTTGTAAAAGCTTATAAATCA
 AATGGTGAGGAAATCAATCTGATGCAAAATACAAATTAGTTATCAATGACTTTTTATTC
 GGTGGTGGTGTGATGGCTTTGCAAGCTTCAGAAATGCCAACTTTAGAGGCAATTAACCCC
 GATACAGAGGTATTATGGCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGC
 GTTCCAATAATAAACCCTAAATCTATGTCACTATGAAGATGGTTAATGAACTATTACA
 CAAAAATGATGGTACACATAGCATTATTAAGAACTTTATTTAGATCGACAAGGAAATATT
 GTAGCAACAAGAGATTGTATCAGACACTTTAAACCAACAAATCAAAATCTACAAAAATC
 AACCCCTGAATCTACAAATTCACAAAAACAATTAACCAATTTACAGCTATTAAACCTATG
 AGAAATTTATGGCAACCATCAAACTCCACTACTGTAAATCAAAACAATTACCAAAAAACA
 AACTCTGAATATGGACAATCATTCCTTATGTCTGTCTTGGTGTGGACTTATAGGAATT
 GCTTTAAATACAAAGAAAAAACATATGAAA

SEQ ID NO. 7102

STRAIN 090

AAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTATGGTGCACCTTGAC
 AATACTGGAACAGCAAAATATGCTGACGGAAGTTACTAATGCTGGCAC
 TGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAAAC
 AAATAACCCCTAATGGTGAAGCATTAGAGTTCAAGCTGGTGATATGGTT
 GGAGCAAGTCCAGCTAACTCAGGGCTTCTCAAGATGAACCAACCGTTAA
 AACATTTAATGCAATGAATGTTGAGTATGGCATTAGGTAACCATGAAT
 TTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAGGCCCT
 GCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGAAGC
 TGCAAAACAGAAATTTAGTGGCAACGTTATTGATAAAGTTAAACAAAC
 AAATCCCTTACAATTTGAAACCTTACGCTATTAAAAATATTCCTGTAAAT
 AACAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAGACATCCC
 AAACCTTGTCTTACGTAAAAATTTATGAACAATATGAATTTTATAGTGAAG
 CTGAAACAATCGTTAAATACGCCAAAGAAATTACAAGCTAAAAATGTCAAG
 GCTATTGTAGTCTTGTCTATGTAACCTGCAACAAGCAAGGATGATATTGC
 TGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCTG
 AAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAAT
 GGTCTTGTGGTAAAACTCGCATTGTACAAGCGCTCTCTCAAGGAAAAGC
 CTATGCTGACGTACGTGGTGTCTTAGATACGTATACACAAGATTTCAATTG
 AAACCCCTTACGCTAAAGTAGTTGAGTGTCTCTGGTAAAAAAGCAGGT
 AGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAACA
 AGTAACAGAAGCTAAATTTGTACTGCCGAGGTAAGTGGCATGATTACGC
 GTTCTGTTGATCAAGATAATGTTAGTCCAGTAGGCGACCTCATCAGAG
 GCTCAACTAGCAATTTGCTCGAAAAAGCTGGCCAGATATCGATTTTGGCCAT
 GACAAATAATGGTGGCATTCTGTGCTGACTTACTCATCAACCAAGATGGAA
 CAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAAATCTTA
 CAAGTCGTGCAAAATTTAGTGGTAGAGATCTTTATAAAGCACTCAACGAACA
 ATACGACCAAAACAAATTTCTTCTTCAAAATAGCTGGTCTGCGATACA
 CTTACACAGATAATAAAGAGGGCGGAGAAAGAAACACCATTTAAAGTTGTA
 AAAGCTTATAAATCAATGGTGAAGAAATCAATCTGATGCAAAATACAA
 ATTAGTTATCAATGACTTTTTATTTCGGTGGTGGTGGTGGCTTTGCAAGCT
 TCAGAAATGCCAAACTCTAGGAGCCATTAAATCCCGATACAGAGGTATT
 ATGGCTTATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGCGTTCC
 AAATAATAAACCTTAAATCTATGTCTACTATGAAGATGGTTAATGAACTA
 TTACACAAATGATGGTACACATAGCATTATTAAGAACTTTATTATGAT
 CGACAAGGAAATATTGTAGCAACAAGAGATTGTATCAGACACTTTAAACCA
 AACAAATCAAAATCTACAAAAATCAACCTGTAACTACAATTCAAAAA
 AACATTAACCAATTTACAGCTATTAAACCTATGAGAAATTATGGCAAA
 CCATCAAACTCCACTACTGTAAATCAAAACA

SEQ ID NO. 7103

STRAIN A909

GCGTCAATGACTTTTATGGTGCCTTGACAACTAGGAAACAGCAAAATATG
 CCTGACGGAAGTTACTAATGCTGGCACTGCTGCTCAATTAGATGCTTA

Table 71: Comparative Sequences relating to SAG1333

TATGGATGATGCTCAAAAAGATTTCAAACAACTAACCTTAATGGTGAAA
GCATTAGAGTTCAAGCTGGTGATATGGTTGGAGCAAGTCCAGCTAACTCA
GGGCTTCTTCAAGATGAACCAACCGTTAAACATTTAATGCAATGAATGT
TGAGTATGGCACATTAGGTAAACCATGAATTTGATGAAGGTTTGGCAGAAT
ACAATCGTATCGTTACTGGAAGGGCCCTGCTCCaGaTTCTAATATAAAT
AATATTACGAAATCATACCCACAGAGCTGCAAAACAAGAAATTTAGT
GGCAAACGTTATTGATAAAGTTAAACAAACAAATCCCTTACAATTGGAAAC
CTTACACTATTAAAAATATTCTGTAAATAACAAAAGTGTGAACGTTGGC
TTTATCGGAATCGTTACCAAGACATCCCAAACTTGTCTTACGTAAAAA
TTATGAACAATATGAATTTTATGATGAAGCTGAAACAAATCGTTAAATACG
CCAAAGAATTACAAGCTAAAAATGTCAAGGCTATTGTAGTCCTTGCTCAT
GTACCTGCAACAAGCAAGGATGATATTGCTGAAGGTGAAGCAGCAGAAAT
GATGAAAAAAGTCAATCAACTCTTCCCTGAAAAATAGCGTAGATATTGTCT
TTGCTGGACACAATCATCAATATACAAATGGTCTTGTGGTAAAACTCGT
ATTGTACAAGCGCTCTCAAGGAAAAGCCTATGCTGATGATCGTGGTGT
CCTAGATACTGATACACAAGATTTCAATTGAAACCCCTTCAGCTAAAGTAA
TTGCAAGTTGCTCTGTTAAAAAAGAGGTAGTGCCGATATTCAAGCCATT
GTTGACCAAGCTAATACTATCGTTAAACAAAGTAACAGAAGCTAAAAATGG
TACTGCCAGGTAAAGTGGCATGATTACGCGTTCTGTTGATCAAGATAATG
TTAGTCCGGTAGGCAGCTCATCACAGAGGCTCAACTAGCAATTGCTCGA
AAAAGCTGGCCAGATATCGATTTTGCCATGACAAATAATGGTGGCATTGG
TGCTGACTTACTCATCAACAGATGGAACAATCACCTGGGGAGCTGCAC
AAGCAGTTCAACCTTTTGGTAATATCTTACAAGTCTGCAAAATTAAGTGT
AGAGATCTTTATAAGCACTCAACGAACAATACGACCAAAAAACAAATTT
CTTCTTCAAATAGCTGGTCTGCGATACACTTACACAGATAATAAAGAGG
GCGGGGAAGAAACACCATTTAAAGTTGTAAGAGCTTATAAATCAAATGGT
GAGGAAATCAATCCTGATGCAAAATACAAATTAGTTATCAATGACTTTTT
ATTGCGTGGTGGTGGTGGCTTTGCAAGCTTCAGAAATGCCAACTCTAG
GAGCCATTAAATCCCGATACAGAGGTATTTATGGCCTATATCACTGATTTA
GAAAAAGCTGGTAAAAAAGTGAAGCTTCCAAATAATAAACCTAAATCTA
TGTCACTATGAAGATGGTTAATGAACCTATTACACAAATGATGGTACAT
ATAGCATTATTAAGAACTTTATTAGATCGACAAGGAAATATTGTAGCA
CAAGAGATTGTATCAGACACTTTAAACCAACAAATCAAATCTACAAA
AATCAACCTGTAACTACAATTACAAAAAACAAATTACACCAATTTACAG
CTATTAAACCTATGAGAAATTTATGGCAACCATCAAACCTCCACTACTGTA
AAATCAAAACAA

SEQ ID NO. 7104

STRAIN H36B

CCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTATGGTGCATTG
ACAATCTGGAACAGCAAATATGCTGACGGAAAAGTTACTAATGCTGGC
ACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAA
ACAAACTAACCTTAATGGTGAAGCATTAGAGTTCAAGCTGGTGAATGG
TTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTT
AAAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATGA
ATTTGATGAAGGTTTGGCAGAATCAATCGTATCGTTACTGGAAAGGCC
CTGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACAGAA
GCTGCAAAACAAGAAATTTGATGTCGCAACGTTATTGATAAAGTTAACAA
ACAAATCCCTTACAAATGGAAACCTTACACTATTAAAAATATTCTGTAA
ATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAGACATC
CCAAACCTTGTCTTACGTAAAAATTTAGAACATATGAATTTTATAGATGA
AGCTGAAACAATCGTTAAATACGCCAAAGAAATTACAAGCTAAAAATGTCA
AGGCTATTGTAGTCCTTGCTCATGTACCTGCAACAAGCAAGGATGATATT
GCTGAAGGTGAAGCAGCAGAAATGATGAAAAAAGTCAATCAACTCTTCCC
TGAAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAA
ATGCTCTTGTGGTAAACTCGTATTGTACAAAGCGCTCTCTCAAGGAAAA
GCCTATGCTGATGATGACGTGGTGTCTTATGATGATGATACACAAGATTCTAT
TGAAACCCCTTCAGCTAAAGTAAATGTCAGTTGCTCTGGTAAAAAAGCAG
GTAGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAA
CAAGTAACAGAAAGCTAAAAATGGTACTGCCGAGGTAAGTGGCATGATTAC
CGCTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCCTCATCACAG
AGGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGGC
ATGACAAATAATGGTGGCATTGCTGCTGACTTACTCATCAACAGATGG
AACATCACTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCT
TACAAGTCGTGAAAAATTAAGTGGTAGAGATCTTTATAAAGCACTCAACGAA
CAATACGACCAAAAAACAAATTTCTTCTTCAAATAGCTGGTCTGCGATA
CACTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCAATTTAAAGTTG
TAAAAGCTTATAAATCAAATGGTGAAGAAATCAATCCTGATGCAAAATAC
AAATTAGTTATCAATGACTTTTATTTCGGTGGTGGTGGTGGCTTTGCAAG
CTTCAGAAATGCCAACTTCTAGGAGCCATTAATCCCGATACAGAGGTAT
TTATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAAGCTT
CCAAATAATAAACCCTAAATCTATGTCATGATGAAGATGGTTAATGAAAC
TATTACAAAAATGATGGTACATATAGCATTTATTAAGAACTTTATTTAG
ATCGACAAGGAAATATTGTAGCACAGAGATTGTATCAGACACTTAAAC
CAACAAAAATCAAATCTACAAAAATCAACCTGTAACTACAATTACAA
AAAACAATTACACCAATTTACAGCTATTAAACCTATGAGAAATTTATGGCA
AACCATCAAACCTCCACTACTGTAATCAAA

SEQ ID NO. 7105

STRAIN 18RS21

GACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTC
ATGGTGCATTGACAATACTGGAACAGCAAATATGCTGACGGAAAAGTT
AnTAATGCTGGCACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCA

Table 71: Comparative Sequences relating to SAG1333

AAAAGATTTCAAACAACTAACCCCTAATGGTGAAAGCATTAGAGTTCAAG
 CTGGTGATATGGTTGGAGCAAGTCCAGCTAACTCAGGCGCTTCTCAAGAT
 GAACCAACCGTTAAACATTTAATGCAATGAATGTTGAGTATGGCACATT
 AGGTAAACCATGAATTTGATGAAGTTTGGCAGAATACAAATCGTATCGTTA
 CTGGAAAGGCCCTGCTCCAGATTCTAATATAAATAATATACGAAATCA
 TACCCACACGAAGCTGCAAAACAAGAAATTTAGTAGGCAACGTTATTGA
 TAAAGTTAAACAAACAAATCCCTTACAATTTGGAACCTTACACTATTAAAA
 ATATTCTCTGTAAATAACAAAGTGTGAACGTTGGCTTTATCGGAATCGTT
 ACCAAAGACATCCCAACCTTGTCTTACGTAAAAATTTATGAACATATGA
 ATTTTTAGATGAAGCTGAACAATCGTTAAATACGCCAAAGAATTACAAG
 CTAAAAATGTCAAGGCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGC
 AAGGATGATATGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAA
 TCAACTCTTCCCTGAAAATAGCGTAGATATTGTCTTGTCTGGACACAATC
 ATCAATATACAAATGGTCTTGTGGTAAACTCGTATTGTACAAGCGCTC
 TCTCAAGGAAAGCCCTATGCTGATGTACGTGGTGTCTTAGATACGTATAC
 ACAAGATTTCATTGAAACCCCTTCAGCTAAAGTAAATGCAAGTTGCTCCTG
 GTAAAAAACAGGTAGTGGCGATATTCAAGCCATTGTTGACCAAGCTAAT
 ACTATCGTTAAACAAGTAACAGAAGCTAAAAATTTGGTACTGCCGAGGTAAG
 TGGCATGATTACGCGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCA
 GCCTCATCACAGAGGCTCAACTAGCAATTTGCTCGAAAAGCTGGCCAGAT
 ATCGATTTTGCCATGACAAATAATGGTGGCATTGCTGCTGACTTACTCAT
 CAAACAGATGGAACAATCACTGGGGAGCTGCACAAGCAGTTCAACCTT
 TTGGTAATATCTTACAAGTCGTGCAAAATTAAGTGGTAGAGATCTTTATAAA
 GCACTCAACGAACAATACGACCAAAACAAAAATTTCTTCTTCAATAGC
 TGGTCTGCGATACACTTACACAGATAATAAGAGGGCGGGGAAGAAACAC
 CATTTAAAGTTGTAAAGCTTATAAATCAAATGGTGAGGAATCAATCCT
 GATGCAAAATACAAATTAGTTATCAATGACTTTTATTTCGGTGGTGGTGA
 TGGCTTTGCAAGCTTCAGAAATGCCAAATTTCTAGGAGCCATTATCCCG
 ATACAGAGGTATTTATGGCCATATATCACTGATTAGAAAAAGCTGGTAAA
 AAGGTAGCGTTCCAAATAATAAACCCTAAATCTATGTCATGATGAAGAT
 GGTTAATGAAACTATTACACAAAATGATGGTACATATAGCATTATTAAGA
 AACTTTATTAGATCGACAAGGAATATTGTAGCACAAGAGATTGTATCA
 GACACTTTAAACCAACAAATCAAATCTACAAAAATCAACCCGTGAAC
 TACAATTACAAAAACAATTAACCAATTTACAGCTATTAAACCTATGA
 GAAATTATGGCAAACCATCAAACTCCACTACTGTAAATCAAAA

SEQ ID NO. 7106

STRAIN M732

ACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACTT
 GACAATACCTGGAACAGCAAAATATGCTGACGGAAGTTACTAATGCTGG
 CACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTC
 AACAACTAACCCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATG
 GTTGAGCAAGTCCAGCTAACTCAGGCGCTTCTTCAAGATGAACCAACCGT
 TAAAAATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATG
 AATTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAGGCC
 CCTGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGA
 AGCTGCAAAACAAGAAATTTAGTGGCAACGTTATTGATAAAGTTAACA
 AACAAATCCCTTACAATTGGAACCTTACACTATTAAAAATATTCTGTGA
 AATAACAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAGACAT
 CCCAAACCTTGTCTTACGTAAAAATTTATGAACAAATATGAATTTTATGATG
 AAGCTGAACAATCGTTAAATACGCAAGAAATTAACAGCTAAAAATGTC
 AAGGCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGCAAGGATGATAT
 TGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCC
 CTGAAAAATAGCGTAGATATTGTCTTGTCTGGACACAATCATCAATATACA
 AATGGTCTTGTGTTGGTAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAA
 AGCCTATGCTGATGTACGTGGTGTCTTAGATACGTATACACAAGATTCA
 TTGAAACCCCTTCAGCTAAAGTAATTGCAAGTTGCTCTCTGGTAAAAAACA
 GGTAGTGCCGATATTCAAGCAATTTGTTGACCAAGCTAATACATCTGTTAA
 ACAAGTAACAGAAGCTAAAAATGGTACTGCCGAGGTAAGTGGCATGATTA
 CGCGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACA
 GAGGCTCAACTAGCAATTTGCTCGAAAAGCTGGCCAGATATCGATTTTGC
 CATGACAAATAATGGTGGCATTGCTGCTGACTTACTCATCAAACAGATG
 GAACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATC
 TTACAAGTCGTGCAATTAAGTGGTAGAGATCTTTATAAGCACTCAACGA
 ACAATACGACCAAAAAACAATAATTTCTTCTTCAATAGCTGGTCTGCGAT
 ACACTTACACAGATAATAAGAGGGCGGGGAAGAAACACCAATTTAAAGTT
 GTAAAGCTTATAAATCAAATGGTGAGGAAATCAATCTGATGCAAAATA
 CAAATTAGTTATCAATGACTTTTATTTCGGTGGTGGTGGTGGCTTTGCAA
 GCTTCAGAAATGCCAACTTCTAGGAGCCATTATCCCGATACAGAGGTA
 TTTATGGCCCTATATCACTGATTAGAAAAAGCTGGTAAAAAAGTGAGCAT
 TCCAAATAATAAACCTAAAAATCTATGTCACTATGAAGATGGTTAATGAAA
 CTATTACAAAAATGATGGTACATATAGCATTATTAAGAAACCTTTATTTA
 GATCGACAAGGAATATTGTAGCACAAGAGATTGTATCAGACACTTTAA
 CCAACAAAAATCAAATCTACAAAAATCAACCCGTGAACCTTACAAATTCACA
 AAAAAAATTAACCAATTTACAGCTATTAAACCTATGAGAAATTATGGC
 AAACCATCAAACTCCACTACTGTAAATCAAAAACA

SEQ ID NO. 7107

STRAIN COH1

ACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACTT
 GACAATACCTGGAACAGCAAAATATGCTGACGGAAGTTACTAATGCTGG
 CACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTC
 AACAACTAACCCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATG

Table 71: Comparative Sequences relating to SAG1333

GT TGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGT
TAAAAACATTAAATGCAATGAATGTTGAGTATGGCACAATTAGGTAACCATG
AATTTGATGAAGTTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCC
CCTGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGA
AGCTGCAAAACAAGAAATTTAGTGGCAACGTTATTGATAAAGTTAACA
AACAAATCCCTTACAATGGGAACCTTACACTATTAAAAATATTCTGTGA
AATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAGACAT
CCCAACCTTGTCTTACGTAATAATATGAACAATATGAATTTTAGATG
AAGCTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTC
AAGGCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGCAAGGATGATAT
TGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCC
CTGAAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACA
AATGGTCTTGTGGTAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAA
AGCCTATGCTGATGTACGTGGTGTCTAGATACGATACACAAGATTTC
TTGAAACCCCTTCAGCTAAAGTAATTGCAGTTGCTCCTGGTAAAAAACA
GGTAGTGCCGATATTCAAGCCATTGTGACCAAGCTAATACTATCGTTAA
ACAAGTAACAGAAAGCTAAAAATGGTACTGCCAGGTAAGTGGCATGATTA
CGCGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACA
GAGGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGC
CATGACAAATAATGGTGGCATTCGTGCTGACTTACTCATCAACCCAGATG
GAACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATC
TTACAAGTCGTGAAATTAAGTGGTAGAGATCTTTATAAAGCACTCAACGA
ACAATACGACCAAAAAACAATAATTTCTTCTCAATAGCTGGTCTGCGAT
ACACTTACACAGATAATAAGAGGGCGGGGAAGAAACACCATTAAAGTT
GTAAAGCTTATAAATCAATGGTGAAGAAATCAATCTGATGCAAAATA
CAAATTAGTTATCAATGACTTTTATTCCGGTGGTGGTGGTGGCTTTGCAA
GCTTCAGAAATGCCAACTTCTAGGAGCCATTATCCGATACAGAGGTA
TTTATGGCCTATATCACTGATTAGAAAAAGCTGGTAAAAAGTGGAGCAT
TCCAAATAATAAACCCTAAAAATCTATGTCACTATGAAGATGGTTAATGAAA
CTATTACACAAATGATGGTACATATAGCATTATTAAGAACTTTATTTA
GATCGACAAGGAAATATGTAGCACAAAGAGATTGTATCAGACACTTTAA
CCAAACAAATCAAAATCTACAAAAATCAACCTGTGAATACAAATTACAA
AAAAACAATTACCAAAATTTACAGCTATTAAACCCTATGAGAAATTATGGC
AAACCATCAAACTCCACTACTGTAAATCAAA

SEQ ID NO. 7108

STRAIN M781

CAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTCATGGTGCACCTTGA
CAATCTGGAACAGCAATATGCCTGACGGAAGTTACTAATGCTGGCA
CTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAGATTTCAAA
CAAACTAACCCCTAATGGTGAAGCATTAGAGTTCAAGCTGGTGGATGGT
TGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTTA
AAACATTTAATGAATGAATGTTGAGTATGGCACAATTAGGTAACCATGAA
TTTGTATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAAGCCCC
TGCTCCAGATTCTAATAATAAATAATATTACGAATCATACCCACACGAAG
CTGCAAAAACAGAAATGTAGTGGCAACGTTATTGATAAAGTTAACAAA
CAAACTCCCTTACAATGGAAACCTTACACTATTAAAAATATTCCTGTAAA
TAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAGACATCC
CAACCTTGTCTTACGTAAAAATTAAGAACAATGAATTTTAGATGAA
GCTGAAACAATCGTTAATAACGCAAGAAATTAAGAAGCTAAAAATGTCAA
GGCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGCAAGGATGATATTG
CTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCT
GAAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAA
TGGTCTTGTGGTAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAG
CCTATGCTGATGTACGTGGTGTCTTAGATACGATACACAAGATTTCATT
GAAACCCCTTCAGCTAAAGTAATTCAGTTGCTCCTGGTAAAAAAGCAGG
TAGTGCCGATATTCAAGCCATTGTGACCAAGCTAATACTATCGTTAAAC
AAGTAACAGAAGCTAAATTTGGTACTGCCAGGTAAGTGGCATGATTACG
CGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGA
GGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGCCA
TGACAAATAATGGTGGCATTCTGTCTGACTTACTCATCAACCCAGATGGA
ACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTT
ACAAGTCGTGAAATTAAGTGGTAGAGATCTTTATAAAGCACTCAACGAAC
AATACGACCAAAAAACAATAATTTCTTCTTCAATAGCTGGTCTGCGATAC
ACTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCATTAAAGTTGT
AAAAGCTTATAAATCAATGGTGAAGAAATCAATCCTGATGCAAAATACA
AATTAGTTATCAATGACTTTTATTCCGGTGGTGGTGGTGGCTTTGCAAGC
TTCAGAAATGCCAACTTCTAGGAGCCATTATCCCGATACAGAGTATT
TATGGCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGGCATTC
CAAAATAAACCCTAAAAATCTATGTCACTATGAAGATGGTTAATGAACT
ATTACAAAAATGATGGTACATATAGCATTATTAAAGAACTTTATTAGTA
TCGACAAGGAAATATTGTAGCACAAAGAGATTGTATCAGACACTTTAAACC
AAACAAAATCAAAATCTACAAAAATCAACCTGTAACTACAATTACAAA
AAACAATTACACCAATTACAGCTATTAAACCCTATGAGAAATTATGGCAA
ACCATCAAACTCCACTACTGTAAATCAAA

SEQ ID NO. 7109

STRAIN CJB110

GACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTCATGGTGC
ACTTGACAATACTGGAACAGCAATATGCCTGACGGAAGAAAGTTACTAATG
CTGGCACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAGAT
TTCAAAACAACTAACCTAATGGTGAAGCATTAGAGTTCAAGCTGGTGA
TATGGTTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAA

Table 71: Comparative Sequences relating to SAG1333

CCGTTAAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAAC
 CATGAATTTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAG
 GGCCCTGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCAC
 ACGAAGCTGCAAAACAGAAATTTAGTGGCAACCGTTATTGATAAAGTT
 AACAAACAAATCCCTTACAATTGGAAACCTTACGCTATTAAAAATATTCC
 TGTAAATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAG
 ACATCCCAACCTTGTCTTACGTAAAAATTTATGAACAATATGAATTTTTTA
 GATGAAGCTGAAACAATCGTTAAATACGCCAAAGAAATTACAAGCTAAAAA
 TGTCAAGGCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGCAAGGATG
 ATATTGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTC
 TTCCTGAAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATA
 TACAAATGGTCTTGTGGTAAAACTCGCATTGTACAAGCGCTCTCTCAAG
 GAAAAGCCTATGCTGACGTACGTGGTGTCTAGATACTGATACACAAGAT
 TTCATTGAAACCCCTTACAGTAAAGTAGTTGCAGTTGCTCCTGGTAAAAA
 AACAGGTAGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATATCTATCG
 TTAACAAGATTAACAGAAGCTAAAAATGGTACTGCCGAGGTAAAGTGGCATG
 ATTACGCGTTCTGTGATCAAGATAATGTTAGTCCAGTAGGCAGCCTCAT
 CACAGAGGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATT
 TTGCCATGACAAATAATGGTGGCATTCTGTGCTGACTTACTCATCAAAACCA
 GATGGAACAATCACCTGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAA
 TATCTTACAAGTCTGTCGAAATTAAGTGGTAGAGATCTTTATAAGCACTCA
 ACGAACATAACGACCAAAAAACAAATTTCTTCTTCAAATAGCTGGTCTG
 CGATACACTTACACAGATAATAAAGAGGGCGGAGAGAAACACCATTTAA
 AGTTGTAAAAGCTTATAAATCAAAATGGTGAAGAAATCAATCCTGATGCAA
 AATACAAATTAGTTATCAATGACTTTTTATTCTGGTGGTGGTATGGCTTT
 GCAAGCTTCAGAAATGCCAACTTCTAGGAGCCATTAAATCCGATACAGA
 GGTATTTATGGCTTATATCACTGATTTAGAAAAAGCTGGTAAAAAGTGA
 GCGTTCCAAATAATAAACCTAAAAATCTATGTCACTATGAAGATGGTTAAT
 GAACTATTACACAAATGATGGTACACATAGCATTATTAAGAACTTTA
 TTTAGATCGACAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTT
 TAAACCAAAACAAATCAAAATCTACAAATCAACCTGTAACTACAAAT
 CACAAAAACAATTACACCAATTTACAGCTATTAACCTATGAGAAATTA
 TGGCAACCATCAAACTCCACTACTGTAAATCA

SEQ ID NO. 7110

STRAIN 1169NT

CAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACCTTGA
 CAATACTGGAACAGCAAAATATGCCCTGATGGAAGAGTTGCTAATGCTGGTA
 CTGCTGCTCAATTAGATGCTTATATGGATGACGCTCAAAAAGATTTCAAA
 CAACTAACCCCTAATGGTGAAGCATTAGGGTTCAAGCAGGCGATATGGT
 TGGAGCAAGTCCAGCCAACTCTGGCTTCTTCAAGATGAACCAACTGTCA
 AAAATTTTAAATGCAATGAATGTTGAGTATGGCAGATTGGGTAAACATGAA
 TTTGATGAAGGGTTGGCAGAAATATAATCGTATCGTTACTGGTAAAGCCCC
 TGCTCCAGATTCTAATATTAATAATATTACGAAATCATACCCACATGAAG
 CTGCAAAACAAGAAATTTAGTGGCAAAATGTTATTGATAAAGTTAACAAA
 CAAATTCCTTACAATTGGAAGCCTTACGCTATTAAAAATATTCCTGTAAA
 TAACAAAGTGTGAACGTTGGCTTTATCGGGATTGTCAACCAAGACATCC
 CAAACCTTGTCTTACGTAAAAATTTATGAACAATATGAATTTTATGATGAA
 GCTGAAACAATCGTTAAATACGCCAAAGAAATTACAAGCTAAAAATGTCAA
 AGCTATTGTAGTCTCGCACATGTACCTGCAACAAGTAAAAATGATATTG
 CTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCT
 GAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAA
 TGGTCTTGTGGTAAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAAG
 CCTATGCTGATGTACGTGGTGTCTTAGATACTGATACACAAGATTTCATT
 GAGACCCCTTCACTAAAGTAATTGCAGTTGCTCCTGGTAAAAAACAGG
 TAGTGCCGATATTCAAGCCATTGTGACCAAGCTAATACTATCGTTAAAC
 AAGTAACAGAAGCTAAAATGGTACTGCCGAGGTAAGTGTATGATTACG
 CGTTCTGTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGA
 GGTCAACTAGCAATTTGCTCGAAAAAGCTGGCCAGATATCGATTTTGCCA
 TGACAAATAATGGTGGCATTCTGTCTGACTTACTCATCAAACCATGGA
 ACAATCACCTGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTT
 ACAAGTCGTGCAAAATTAAGTAGAGATCTTTATAAGCACTCAACGAAC
 AATACGACCAAAAAACAAATTTCTTCTTCAAATAGCTGGTCTGCGATAC
 ACTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTTGT
 AAAAGCTTATAAATCAAAATGGTGAAGGAAATCAATCCTGATGCAAAATACA
 AATTAGTTATCAATGACTTTTATTCTGGTGGTGGTATGGCTTTGCAAGC
 TTCAGAAATGCCAACTTCTAGGAGCCATTAAACCCGATACAGAGGTATT
 TATGGCCTATATCACTGATTAGAAAAAGCTGGTAAAAAGTGAAGCGTTT
 CAAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTTAATGAACT
 ATTACACAAAATGATGGTACACATAGCATTATTAAGAACTTTATTTAGA
 TCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAACC
 AAACAAATCAAAATCTACAAAAATCAACCTGTAACTACAAATCACAAA
 AAACAATTACACCAATTTACAGCTATTAACCTATGAGAAATTTAGCAA
 ACCATCAAACTCCACTACTGTAAATCAAA

SEQ ID NO. 7111

STRAIN JM9130013

CGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACCTTGACAATA
 CTGGAACAGCAAAATATGCCCTGACGGAAGGTTACTAATGCTGGCACTGCT
 GCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAAACAAAC
 TAACCCTAATGGTGAAGCATTAGAGTTCAAGCTGGTGGTATGGTTGGAG
 CAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTTAAACCA
 TTTAATGCAATGAATGTTGAGTATGGCAGATTAGGTAAACATGAATTTGA

Table 71: Comparative Sequences relating to SAG1333

TGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCCCTGCTC
 CAGATTcTAATATAAATAATATTACGAAATCATACCCACACGAAGCTGCA
 AAACAAGAAATTTAGTGGCAACGTTATTGATAAAGTTAAACAAACAAAT
 CCCTTACAATTTGGAACCTTACACTATTAAAAATATTCTGTAAATAACA
 AAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAGACATCCCAAAC
 CTGTCTTACGTAAAAATTATGAACAATATGAATTTTATAGATGAAGCTGA
 AACAAATCGTTAAATACGCCAAAGAATTACAGCTAAAAATGTCAAGGCTA
 TTGTAGTCTTGTCTCATGTACCTGCAACAGCAAGGATGATATTGCTGAA
 GGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCTGAAAA
 TAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAATGGTC
 TTGTTGGTAAAACTCGTATTGTACAGCGCTCTCTCAAGGAAAAGCCTAT
 GCTGATGTACGTGGTGTCTAGATACCTGATACACAAGATTTTATTGAAAC
 CCCTTCAGCTAAAGTAATTGCAAGTTGCTCTGTTAAAAAACAGGTAGTG
 CCGATATTCAAGCAATTCTTGACCAAGCTAATACTATCGTTAAACAAGTA
 ACAGAAGCTAAAAATTTGTTACTGCGGAGGTAAAGTGGCATGATTACGCGTTC
 TGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGAGGCTC
 AACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGCCATGACA
 AATAATGGTGGCATTCTGTCTGACTTACTCATCAAACAGATGGAACAAT
 CACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTTACAAG
 TCGTCAAAATTAATGTTAGATCTTTATAAAGCACTCAACGAACAATAC
 GACCAAAAAACAAATTTCTTCTTCAAAATAGCTGGTCTGCGATACACTTA
 CACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTTGTAAAG
 CTTATAAATCAAAATGGTGAAGAAATCAATCCTGATGCAAAATACAAATTA
 GTTATCAATGACTTTTATTCTGTTGGTGGTGGTGGCTTTGCAAGCTTCAG
 AAATGCCAACTCTTAGGAGCCATTAATCCCGATACAGAGGTATTATGG
 CCTATATCACTGATTAGAAAAAGCTGGTAAAAAGTGAGCGTTCCAAT
 AATAAACCTAAAACTATGTCTACTATGAAGATGGTTAATGAACTATTAC
 ACAAAATGATGGTACATATAGCAATTATTGAGAACTTTATTATAGATCGAC
 AAGGAAATATTGTAGCACAAAGAGATTGTATCAGACACTTTAAACCAAACA
 AAATCAAAATCTACAAAATCAACCTGTAACCTACAATTACAAAAAACA
 ATTACCAATTTACAGCTATTAAACCTATGAGAAATTTATGGCAACCAT
 CAACTCCACTACTGTAAATCAAAA

PRETTY of: /biotmp/msa237456.2{*} May 14, 2003 03:20 ..

	1				50
msa237456.2{328_1169NT}	-----	-----	-----	-----	-----
msa237456.2{328_2603}	atgaaaaaga	aaattattht	gaaaagtagt	gttcttggtt	tagtcgctgg
msa237456.2{328_18RS21}	-----	-----	-----	-----	-----
msa237456.2{328_H36B}	-----	-----	-----	-----	-----
msa237456.2{328_COH1}	-----	-----	-----	-----	-----
msa237456.2{328_M732}	-----	-----	-----	-----	-----
msa237456.2{328_M781}	-----	-----	-----	-----	-----
msa237456.2{328_JM9130013}	-----	-----	-----	-----	-----
msa237456.2{328_A909}	-----	-----	-----	-----	-----
msa237456.2{328_090}	-----	-----	-----	-----	-----
msa237456.2{328_CJB110}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa237456.2{328_1169NT}	-----	-----	-----	-----	-----
msa237456.2{328_2603}	gacttctatt	atgttctcaa	gcgtgttcgc	gGACcaagtc	ggtgtccaag
msa237456.2{328_18RS21}	-----	-----	-----	-----	-----
msa237456.2{328_H36B}	-----	-----	-----	-----	-----
msa237456.2{328_COH1}	-----	-----	-----	-----	-----
msa237456.2{328_M732}	-----	-----	-----	-----	-----
msa237456.2{328_M781}	-----	-----	-----	-----	-----
msa237456.2{328_JM9130013}	-----	-----	-----	-----	-----
msa237456.2{328_A909}	-----	-----	-----	-----	-----
msa237456.2{328_090}	-----	-----	-----	-----	-----
msa237456.2{328_CJB110}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	101				150
msa237456.2{328_1169NT}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_2603}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_18RS21}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_H36B}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_COH1}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_M732}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_M781}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_JM9130013}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_A909}	-----GCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_090}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_CJB110}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
Consensus	-----****	*****	*****	*****	*****
	151				200
msa237456.2{328_1169NT}	AATATGCCTG	AtGGAAAAAGT	TgcTAATGCT	GGtACTGCTG	CTCAATTAGA
msa237456.2{328_2603}	AATATGCCTG	AtGGAAAAAGT	TgcTAATGCT	GGtACTGCTG	CTCAATTAGA
msa237456.2{328_18RS21}	AATATGCCTG	AcGGAAAAAGT	TanTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_H36B}	AATATGCCTG	AcGGAAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_COH1}	AATATGCCTG	AcGGAAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_M732}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_M781}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_JM9130013}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_A909}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_CJB110}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
Consensus	*****	*-*****	*-*****	*-*****	*****
msa237456.2{328_1169NT}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_2603}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_18RS21}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_H36B}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_COH1}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_M732}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_M781}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_JM9130013}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_A909}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_090}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_CJB110}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_2603}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_18RS21}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_H36B}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_COH1}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_M732}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_M781}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_JM9130013}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_A909}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_090}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_CJB110}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_2603}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_18RS21}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_H36B}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_COH1}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_M732}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_M781}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_JM9130013}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_A909}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_090}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_CJB110}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_2603}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_18RS21}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_H36B}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_COH1}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_M732}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_M781}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_JM9130013}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_A909}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_090}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_CJB110}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGtTTGG
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	CAGAATAcAA	TCGTATCGTT	ACTGGtAAAg	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_2603}	CAGAATAcAA	TCGTATCGTT	ACTGGtAAAg	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_18RS21}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_H36B}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_COH1}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_M732}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_M781}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_JM9130013}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_A909}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_090}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_CJB110}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	ATtAATAATA	TTACGAAATC	ATACCCACat	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_2603}	ATtAATAATA	TTACGAAATC	ATACCCACat	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_18RS21}	ATaAATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_H36B}	ATaAATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_COH1}	ATAATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT		
msa237456.2{328_M732}	ATAATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT		
msa237456.2{328_M781}	ATAATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT		
msa237456.2{328_JM9130013}	ATAATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT		
msa237456.2{328_A909}	ATAATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT		
msa237456.2{328_090}	ATAATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT		
msa237456.2{328_CJB110}	ATAATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT		
Consensus	*****	*****	*****	*****	*****		
msa237456.2{328_1169NT}	501	TGTTAGTGGCA	AATGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT	550
msa237456.2{328_2603}	TGTTAGTGGCA	AATGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT		
msa237456.2{328_18RS21}	TGTTAGTGGCA	AACGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT		
msa237456.2{328_H36B}	TGTTAGTGGCA	AACGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT		
msa237456.2{328_COH1}	TGTTAGTGGCA	AACGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT		
msa237456.2{328_M732}	TGTTAGTGGCA	AACGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT		
msa237456.2{328_M781}	TGTTAGTGGCA	AACGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT		
msa237456.2{328_JM9130013}	TGTTAGTGGCA	AACGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT		
msa237456.2{328_A909}	TGTTAGTGGCA	AACGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT		
msa237456.2{328_090}	TGTTAGTGGCA	AACGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT		
msa237456.2{328_CJB110}	TGTTAGTGGCA	AACGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT		
Consensus	*****	**_*****	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	551	GGAAgCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC	600
msa237456.2{328_2603}	GGAAgCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC		
msa237456.2{328_18RS21}	GGAAaCCTTA	CaCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC		
msa237456.2{328_H36B}	GGAAaCCTTA	CaCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC		
msa237456.2{328_COH1}	GGAAaCCTTA	CaCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC		
msa237456.2{328_M732}	GGAAaCCTTA	CaCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC		
msa237456.2{328_M781}	GGAAaCCTTA	CaCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC		
msa237456.2{328_JM9130013}	GGAAaCCTTA	CaCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC		
msa237456.2{328_A909}	GGAAaCCTTA	CaCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC		
msa237456.2{328_090}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC		
msa237456.2{328_CJB110}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC		
Consensus	*****	*_*****	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	601	GTTGGCTTTA	TCGGgATtGT	cACCAAGAC	ATCCCAAACC	TTGTCTTACG	650
msa237456.2{328_2603}	GTTGGCTTTA	TCGGgATtGT	cACCAAGAC	ATCCCAAACC	TTGTCTTACG		
msa237456.2{328_18RS21}	GTTGGCTTTA	TCGGaATcGT	tACCAAGAC	ATCCCAAACC	TTGTCTTACG		
msa237456.2{328_H36B}	GTTGGCTTTA	TCGGaATcGT	tACCAAGAC	ATCCCAAACC	TTGTCTTACG		
msa237456.2{328_COH1}	GTTGGCTTTA	TCGGaATcGT	tACCAAGAC	ATCCCAAACC	TTGTCTTACG		
msa237456.2{328_M732}	GTTGGCTTTA	TCGGaATcGT	tACCAAGAC	ATCCCAAACC	TTGTCTTACG		
msa237456.2{328_M781}	GTTGGCTTTA	TCGGaATcGT	tACCAAGAC	ATCCCAAACC	TTGTCTTACG		
msa237456.2{328_JM9130013}	GTTGGCTTTA	TCGGaATcGT	tACCAAGAC	ATCCCAAACC	TTGTCTTACG		
msa237456.2{328_A909}	GTTGGCTTTA	TCGGaATcGT	tACCAAGAC	ATCCCAAACC	TTGTCTTACG		
msa237456.2{328_090}	GTTGGCTTTA	TCGGaATcGT	tACCAAGAC	ATCCCAAACC	TTGTCTTACG		
msa237456.2{328_CJB110}	GTTGGCTTTA	TCGGaATcGT	tACCAAGAC	ATCCCAAACC	TTGTCTTACG		
Consensus	*****	*****_**_**	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	651	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA	700
msa237456.2{328_2603}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA		
msa237456.2{328_18RS21}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA		
msa237456.2{328_H36B}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA		
msa237456.2{328_COH1}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA		
msa237456.2{328_M732}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA		
msa237456.2{328_M781}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA		
msa237456.2{328_JM9130013}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA		
msa237456.2{328_A909}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA		
msa237456.2{328_090}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA		
msa237456.2{328_CJB110}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA		
Consensus	*****	*****	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	701	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTc	750
msa237456.2{328_2603}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTc		
msa237456.2{328_18RS21}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAgGCTAT	TGTAGTcCTt		
msa237456.2{328_H36B}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAgGCTAT	TGTAGTcCTt		
msa237456.2{328_COH1}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAgGCTAT	TGTAGTcCTt		
msa237456.2{328_M732}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAgGCTAT	TGTAGTcCTt		
msa237456.2{328_M781}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAgGCTAT	TGTAGTcCTt		
msa237456.2{328_JM9130013}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAgGCTAT	TGTAGTcCTt		
msa237456.2{328_A909}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAgGCTAT	TGTAGTcCTt		
msa237456.2{328_090}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAgGCTAT	TGTAGTcCTt		
msa237456.2{328_CJB110}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAgGCTAT	TGTAGTcCTt		
Consensus	*****	*****	*****	*****	*****_**_**	*****	*****
msa237456.2{328_1169NT}	751	GCaCATGTAC	CTGCAACAAG	tAAaaATGAT	ATTGCTGAAG	GTGAAGCAGC	800
msa237456.2{328_2603}	GCaCATGTAC	CTGCAACAAG	tAAaaATGAT	ATTGCTGAAG	GTGAAGCAGC		
msa237456.2{328_18RS21}	GcTcATGTAC	CTGCAACAAG	cAaggATGAT	ATTGCTGAAG	GTGAAGCAGC		

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_H36B}	GctCATGTAC	CTGCAACAAG	cAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_COH1}	GctCATGTAC	CTGCAACAAG	cAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_M732}	GctCATGTAC	CTGCAACAAG	cAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_M781}	GctCATGTAC	CTGCAACAAG	cAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_JM9130013}	GctCATGTAC	CTGCAACAAG	cAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_A909}	GctCATGTAC	CTGCAACAAG	cAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_O90}	GctCATGTAC	CTGCAACAAG	cAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_CJB110}	GctCATGTAC	CTGCAACAAG	cAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
Consensus	***-*****	*****-***	*****-***	*****-***	*****-***
msa237456.2{328_1169NT}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_2603}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_18RS21}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_H36B}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_COH1}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_M732}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_M781}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_JM9130013}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_A909}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_O90}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_CJB110}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
Consensus	*****-***	*****-***	*****-***	*****-***	*****-***
msa237456.2{328_1169NT}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_2603}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_18RS21}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_H36B}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_COH1}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_M732}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_M781}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_JM9130013}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_A909}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_O90}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_CJB110}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
Consensus	*****-***	*****-***	*****-***	*****-***	*****-***
msa237456.2{328_1169NT}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGatGTACG
msa237456.2{328_2603}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGatGTACG
msa237456.2{328_18RS21}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGatGTACG
msa237456.2{328_H36B}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGatGTACG
msa237456.2{328_COH1}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGatGTACG
msa237456.2{328_M732}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGatGTACG
msa237456.2{328_M781}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGatGTACG
msa237456.2{328_JM9130013}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGatGTACG
msa237456.2{328_A909}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGatGTACG
msa237456.2{328_O90}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGatGTACG
msa237456.2{328_CJB110}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGatGTACG
Consensus	*****-***	*****-***	*****-***	*****-***	*****-***
msa237456.2{328_1169NT}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_2603}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_18RS21}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_H36B}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_COH1}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_M732}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_M781}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_JM9130013}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_A909}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_O90}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_CJB110}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
Consensus	*****-***	*****-***	*****-***	*****-***	*****-***
msa237456.2{328_1169NT}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_2603}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_18RS21}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_H36B}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_COH1}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_M732}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_M781}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_JM9130013}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_A909}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_O90}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_CJB110}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
Consensus	*****-***	*****-***	*****-***	*****-***	*****-***
msa237456.2{328_1169NT}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_2603}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_18RS21}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_H36B}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_COH1}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_M732}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_M781}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_JM9130013}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_A909}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_090}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_CJB110}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	AATTGGTACT	GCCGAGGTAA	GTGtCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_2603}	AATTGGTACT	GCCGAGGTAA	GTGtCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_18RS21}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_H36B}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_COH1}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_M732}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_M781}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_JM9130013}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_A909}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_090}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_CJB110}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
Consensus	*****	*****	***_*****	*****	*****
msa237456.2{328_1169NT}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_2603}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_18RS21}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_H36B}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_COH1}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_M732}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_M781}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_JM9130013}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_A909}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_090}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_CJB110}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
Consensus	*****	***_*****	*****	*****	*****
msa237456.2{328_1169NT}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_2603}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_18RS21}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_H36B}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_COH1}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_M732}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_M781}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_JM9130013}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_A909}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_090}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_CJB110}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_2603}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_18RS21}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_H36B}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_COH1}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_M732}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_M781}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_JM9130013}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_A909}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_090}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_CJB110}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_2603}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_18RS21}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_H36B}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_COH1}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_M732}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_M781}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_JM9130013}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_A909}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_090}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_CJB110}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	ACTGGTAGAG	ATCTTTTATA	AGCACTCAAC	GAACAATACG	ACCAAAAACA
	1351				1400

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_1169NT}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_2603}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_18RS21}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_H36B}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_COH1}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	aTTCCAAATA	ATAAACCTAA
msa237456.2{328_M732}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	aTTCCAAATA	ATAAACCTAA
msa237456.2{328_M781}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	aTTCCAAATA	ATAAACCTAA
msa237456.2{328_JM9130013}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_A909}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_090}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_CJB110}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
Consensus	*****	*****	*****	-*****	*****
msa237456.2{328_1169NT}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_2603}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_18RS21}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_H36B}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_COH1}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_M732}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_M781}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_JM9130013}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_A909}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_090}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_CJB110}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_2603}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_18RS21}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_H36B}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_COH1}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_M732}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_M781}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_JM9130013}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_A909}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_090}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_CJB110}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_2603}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_18RS21}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_H36B}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_COH1}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_M732}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_M781}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_JM9130013}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_A909}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_090}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_CJB110}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_2603}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_18RS21}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_H36B}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_COH1}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_M732}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_M781}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_JM9130013}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_A909}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_090}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_CJB110}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_2603}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_18RS21}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_H36B}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_COH1}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_M732}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_M781}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_JM9130013}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_A909}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_090}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_CJB110}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
Consensus	*****	*****	*****	*****	*****

Table 71: Comparative Sequences relating to SAG1333

	1951			2000
msa237456.2{328_1169NT}	ACTGTAAAT CAaa-----	-----	-----	-----
msa237456.2{328_2603}	ACTGTAAAT CAaaACAAtt	acaaaaaaca	aactctgaat	atggacaatc
msa237456.2{328_18RS21}	ACTGTAAAT CAaaA-----	-----	-----	-----
msa237456.2{328_H36B}	ACTGTAAAT CAaa-----	-----	-----	-----
msa237456.2{328_COH1}	ACTGTAAAT CAaa-----	-----	-----	-----
msa237456.2{328_M732}	ACTGTAAAT CAaaACAA--	-----	-----	-----
msa237456.2{328_M781}	ACTGTAAAT CAaa-----	-----	-----	-----
msa237456.2{328_JM9130013}	ACTGTAAAT CAaaA-----	-----	-----	-----
msa237456.2{328_A909}	ACTGTAAAT CAaaACAA--	-----	-----	-----
msa237456.2{328_090}	ACTGTAAAT CAaaACAA--	-----	-----	-----
msa237456.2{328_CJB110}	ACTGTAAAT CA-----	-----	-----	-----
Consensus	***** **_*****	*****	*****	*****
	2001			2050
msa237456.2{328_1169NT}	-----	-----	-----	-----
msa237456.2{328_2603}	attccttatg	tctgtctttg	gtgttggaact	tataggaatt
msa237456.2{328_18RS21}	-----	-----	-----	-----
msa237456.2{328_H36B}	-----	-----	-----	-----
msa237456.2{328_COH1}	-----	-----	-----	-----
msa237456.2{328_M732}	-----	-----	-----	-----
msa237456.2{328_M781}	-----	-----	-----	-----
msa237456.2{328_JM9130013}	-----	-----	-----	-----
msa237456.2{328_A909}	-----	-----	-----	-----
msa237456.2{328_090}	-----	-----	-----	-----
msa237456.2{328_CJB110}	-----	-----	-----	-----
Consensus	*****	*****	*****	*****
	2051			2070
msa237456.2{328_1169NT}	-----	-----	-----	-----
msa237456.2{328_2603}	caaagaaaaa	acatatgaaa	-----	-----
msa237456.2{328_18RS21}	-----	-----	-----	-----
msa237456.2{328_H36B}	-----	-----	-----	-----
msa237456.2{328_COH1}	-----	-----	-----	-----
msa237456.2{328_M732}	-----	-----	-----	-----
msa237456.2{328_M781}	-----	-----	-----	-----
msa237456.2{328_JM9130013}	-----	-----	-----	-----
msa237456.2{328_A909}	-----	-----	-----	-----
msa237456.2{328_090}	-----	-----	-----	-----
msa237456.2{328_CJB110}	-----	-----	-----	-----
Consensus	*****	*****	-----	-----

SEQ ID NO. 7112

STRAIN 2603 frame: 1

MKKKIILKSSVLGLVAGTSIMFSSVFADQVGQVIGVNDVFGALDNTGTANMPDGKVVANA
 GTAAQLDAYMDDAQDKFKQTNPNGESIRVQAGDMVGASPANSGLLQDEPTVKNFNAMNVE
 YGTLGNHEFDEGLAEYNIIVTGKAPAPDSNINNTKSYPHAAKQEIIVVANVIDKVNKQI
 PYNWKPYAIKNI PVNNKSVNVGFIGIVTKDIPNLVLRKNYBQYEFLEDEAETIVKYAKELQ
 AKNVKAIIVLAHVPAATSKNDIAEGEAAEMMKVNLFPENSVDIVFAGHNHQTNGLVGK
 TRIVQALSQGGKAYADVRGVLDTDTQDFIETPSAKVIAVAPGKKTGSADIQAIQVQANTIV
 KQVTEAKIGTAEVSMITRSVDQDNVSPVGLSLITEAQLAIARKSWPIDFAMTNNGGIRAD
 LLIKPDGTITWGAAQAVQPFNGILQVVEITGRDLYKALNEQYDQKQNFLLQIAGLRYTY
 TDNKEGGEETPFKVVKAYKSNGBEINPDACYKLVINDFLFGGGDGFASFRNAKLLGAINP
 DTEVFMAIYITDLEKAGKKVSVPNKPKIYVTMKNVNETITQNDGTHSIIKKLYLDRQGN
 VAQEIVSDTLNQTQKSKSTKINPVTTIHKQLHQFTA INPMRNYGKPSNSTTVKSKQLPKT
 NSEYQGSFLMSVFGVGLIGIALNTKKKHKM

SEQ ID NO. 7113

STRAIN 090 frame: 3

VGVQVIGVNDVFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQDKFKQTNPNGESIRV
 QAGDMVGASPANSGLLQDEPTVKTNFAMNVEYGTGNGHEFDEGLAEYNIIVTGKAPAPDS
 NINNTKSYPHAAKQEIIVVANVIDKVNKQIPYNWKPYAIKNI PVNNKSVNVGFIGIVTK
 DIPNLVLRKNYBQYEFLEDEAETIVKYAKELQAKNVKAIIVLAHVPAATSKDDIAEGEAAEM
 MKVNLFPENSVDIVFAGHNHQTNGLVGKTRIVQALSQGGKAYADVRGVLDTDTQDFIET
 PSKAVVAVAPGKKTGSADIQAIQVQANTIVKQVTEAKIGTAEVSMITRSVDQDNVSPV
 GSLITEAQLAIARKSWPIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFNGILQVVE
 ITGRDLYKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGBEINPD
 KYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIYITDLEKAGKKVSVPNKPKIY
 VTMKNVNETITQNDGTHSIIKKLYLDRQGNIVAQEIVSDTLNQTQKSKSTKINPVTTIHK
 QLHQFTA INPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7114

STRAIN A909 frame: 3

VNDVFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQDKFKQTNPNGESIRVQAGDMVG
 ASPANSGLLQDEPTVKTNFAMNVEYGTGNGHEFDEGLAEYNIIVTGKAPAPDSNINNTK
 SYPHAAKQEIIVVANVIDKVNKQIPYNWKPYTIKNI PVNNKSVNVGFIGIVTKDIPNLV
 RKNYBQYEFLEDEAETIVKYAKELQAKNVKAIIVLAHVPAATSKDDIAEGEAAEMMKVNL
 FPENSVDIVFAGHNHQTNGLVGKTRIVQALSQGGKAYADVRGVLDTDTQDFIETPSAKVI
 AVAPGKKTGSADIQAIQVQANTIVKQVTEAKIGTAEVSMITRSVDQDNVSPVGLSLITEA
 QLAIAARKSWPIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFNGILQVVEITGRDLY
 KALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGBEINPDACYKLVIN
 DFLFGGGDGFASFRNAKLLGAINPDTEVFMAIYITDLEKAGKKVSVPNKPKIYVTMKNV
 ETITQNDGTHSIIKKLYLDRQGNIVAQEIVSDTLNQTQKSKSTKINPVTTIHKQLHQFTA

Table 71: Comparative Sequences relating to SAG1333

INPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7115

STRAIN H36B frame: 2

QVGQVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKTFFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAPD
 SNINNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIVT
 KDI PNLVLRKNYEQYEFLEDAETIVKYAKELQAKNVKAI VVLAHVPAATSKDDIAEGEAAE
 MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQKAYADVRGVLDTDQDFI
 ETPSAKVIAVAPGKKTGSADIQAI VQDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLIKPDGTITWGAAQAVQPPFNILQV
 EITGRDLYKALNEQYDQKQNFLLQIAGLRITYTNDKEGGEETPFKVVKAYKSNGEIINPD
 AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKVSVPNNKPKI
 YVTMKNVNETITQNDGTYSIIKKLYLDRQGNIVAQEI VSDTLNQTQKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7116

STRAIN 18RS21 frame: 1

DQVGQVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 RVQAGDMVGASPANSGLLQDEPTVKTFFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAP
 DSNINNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIV
 TKDI PNLVLRKNYEQYEFLEDAETIVKYAKELQAKNVKAI VVLAHVPAATSKDDIAEGEAAE
 EMMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQKAYADVRGVLDTDQDFI
 IETPSAKVIAVAPGKKTGSADIQAI VQDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 PVGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLIKPDGTITWGAAQAVQPPFNILQV
 VEITGRDLYKALNEQYDQKQNFLLQIAGLRITYTNDKEGGEETPFKVVKAYKSNGEIINPD
 DAKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKVSVPNNKPKI
 IYVTMKNVNETITQNDGTYSIIKKLYLDRQGNIVAQEI VSDTLNQTQKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKSK

SEQ ID NO. 7117

STRAIN M732 frame: 3

QVGQVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKTFFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAPD
 SNINNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIVT
 KDI PNLVLRKNYEQYEFLEDAETIVKYAKELQAKNVKAI VVLAHVPAATSKDDIAEGEAAE
 MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQKAYADVRGVLDTDQDFI
 ETPSAKVIAVAPGKKTGSADIQAI VQDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLIKPDGTITWGAAQAVQPPFNILQV
 EITGRDLYKALNEQYDQKQNFLLQIAGLRITYTNDKEGGEETPFKVVKAYKSNGEIINPD
 AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKVSVPNNKPKI
 YVTMKNVNETITQNDGTYSIIKKLYLDRQGNIVAQEI VSDTLNQTQKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7118

STRAIN COH1 frame: 3

QVGQVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKTFFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAPD
 SNINNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIVT
 KDI PNLVLRKNYEQYEFLEDAETIVKYAKELQAKNVKAI VVLAHVPAATSKDDIAEGEAAE
 MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQKAYADVRGVLDTDQDFI
 ETPSAKVIAVAPGKKTGSADIQAI VQDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLIKPDGTITWGAAQAVQPPFNILQV
 EITGRDLYKALNEQYDQKQNFLLQIAGLRITYTNDKEGGEETPFKVVKAYKSNGEIINPD
 AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKVSVPNNKPKI
 YVTMKNVNETITQNDGTYSIIKKLYLDRQGNIVAQEI VSDTLNQTQKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7119

STRAIN M781 frame: 1

QVGQVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKTFFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAPD
 SNINNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIVT
 KDI PNLVLRKNYEQYEFLEDAETIVKYAKELQAKNVKAI VVLAHVPAATSKDDIAEGEAAE
 MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQKAYADVRGVLDTDQDFI
 ETPSAKVIAVAPGKKTGSADIQAI VQDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLIKPDGTITWGAAQAVQPPFNILQV
 EITGRDLYKALNEQYDQKQNFLLQIAGLRITYTNDKEGGEETPFKVVKAYKSNGEIINPD
 AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKVSVPNNKPKI
 YVTMKNVNETITQNDGTYSIIKKLYLDRQGNIVAQEI VSDTLNQTQKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7120

STRAIN CJB110 frame: 1

DQVGQVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 RVQAGDMVGASPANSGLLQDEPTVKTFFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAP
 DSNINNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIV
 TKDI PNLVLRKNYEQYEFLEDAETIVKYAKELQAKNVKAI VVLAHVPAATSKDDIAEGEAAE
 EMMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQKAYADVRGVLDTDQDFI
 IETPSAKVIAVAPGKKTGSADIQAI VQDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 PVGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLIKPDGTITWGAAQAVQPPFNILQV
 VEITGRDLYKALNEQYDQKQNFLLQIAGLRITYTNDKEGGEETPFKVVKAYKSNGEIINPD

Table 71: Comparative Sequences relating to SAG1333

DAKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVPNKPK
IYVTMKNVNETITQNDGTHSI IKKLYLDRQGNIVAQEIVSDTLNQTSKSTKINPVTTH
KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7121

STRAIN 1169NT frame: 1

QVGQVIGVNDHFHGLDNTGTANMPDGKVNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
VQAGDMVGASPDNSGLLQDEPTVKFNAMNVEYGTIGNHEFDEGLAEYNRIVTGKAPAPD
SNINNITKSPHEAAKQEIIVANVIDKVNKQIPYNWKPYAIKNI PVNNKSVNVGFIGIVT
KDI PNVLVRKNYEQYEFLEAETI VKYAKELQAKNVKAI VVLAHV PATSKND IAEGEAAE
MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRI VQALSQGKAYADVRGVLDTDQDFI
ETPSAKVIAVAPGKKTGSADIQAI VDOQANTIVKQVTEAKIGTAEVSMITRSVDQDNVSP
VGSLLITEAQLAIARKSWPIDFAMTNNGGIRADLLIKPDGTITWGAQAQVQFPGNQLQV
EITGRDLKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKA YKSNGEIINPD
AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVPNKPKI
YVTMKNVNETITQNDGTHSI IKKLYLDRQGNIVAQEIVSDTLNQTSKSTKINPVTTHK
KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7122

STRAIN JM9130013 frame: 2

GVQVIGVNDHFHGLDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRVQ
AGDMVGASPDNSGLLQDEPTVKFNAMNVEYGTIGNHEFDEGLAEYNRIVTGKAPAPDSN
INNITKSPHEAAKQEIIVANVIDKVNKQIPYNWKPYTIKNI PVNNKSVNVGFIGIVTKD
IPNLVLRKNYEQYEFLEAETI VKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAAEM
KKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRI VQALSQGKAYADVRGVLDTDQDFIET
PSAKVIAVAPGKKTGSADIQAI VDOQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSPV
SLITEAQLAIARKSWPIDFAMTNNGGIRADLLIKPDGTITWGAQAQVQFPGNQLQVIE
TGRDLKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKA YKSNGEIINPD
YKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVPNKPKIYV
TMKNVNETITQNDGTHSI IKKLYLDRQGNIVAQEIVSDTLNQTSKSTKINPVTTHKKQ
LHQFTAINPMRNYGKPSNSTTVKS

PRETTY of: /biotmp/msa237615.2{*} May 14, 2003 03:22 ..

	i		50
msa237615.2{328_1169NT}	-----	-----qv	gvqvigVNDF HGALDNTGTA
msa237615.2{328_2603}	mkkkilkss	vlglvagtsi	mfssvfadqv gvqvigVNDF HGALDNTGTA
msa237615.2{328_A909}	-----	-----	-----VNDF HGALDNTGTA
msa237615.2{328_M732}	-----	-----qv	gvqvigVNDF HGALDNTGTA
msa237615.2{328_COH1}	-----	-----qv	gvqvigVNDF HGALDNTGTA
msa237615.2{328_M781}	-----	-----qv	gvqvigVNDF HGALDNTGTA
msa237615.2{328_H36B}	-----	-----qv	gvqvigVNDF HGALDNTGTA
msa237615.2{328_JM9130013}	-----	-----	gvqvigVNDF HGALDNTGTA
msa237615.2{328_18RS21}	-----	-----Dqv	gvqvigVNDF HGALDNTGTA
msa237615.2{328_090}	-----	-----v	gvqvigVNDF HGALDNTGTA
msa237615.2{328_CJB110}	-----	-----Dqv	gvqvigVNDF HGALDNTGTA
Consensus	*****	*****	*****
	51		100
msa237615.2{328_1169NT}	NMPDGKvNA	GTAQAQLDAYM	DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
msa237615.2{328_2603}	NMPDGKvNA	GTAQAQLDAYM	DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
msa237615.2{328_A909}	NMPDGKvNA	GTAQAQLDAYM	DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
msa237615.2{328_M732}	NMPDGKvNA	GTAQAQLDAYM	DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
msa237615.2{328_COH1}	NMPDGKvNA	GTAQAQLDAYM	DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
msa237615.2{328_M781}	NMPDGKvNA	GTAQAQLDAYM	DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
msa237615.2{328_H36B}	NMPDGKvNA	GTAQAQLDAYM	DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
msa237615.2{328_JM9130013}	NMPDGKvNA	GTAQAQLDAYM	DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
msa237615.2{328_18RS21}	NMPDGKvNA	GTAQAQLDAYM	DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
msa237615.2{328_090}	NMPDGKvNA	GTAQAQLDAYM	DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
msa237615.2{328_CJB110}	NMPDGKvNA	GTAQAQLDAYM	DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
Consensus	*****	*****	*****
	101		150
msa237615.2{328_1169NT}	NSGLLQDEPT	VKnFNAMNVE	YGTIGNHEFD EGLAEYNRIV TGKAPAPDSN
msa237615.2{328_2603}	NSGLLQDEPT	VKnFNAMNVE	YGTIGNHEFD EGLAEYNRIV TGKAPAPDSN
msa237615.2{328_A909}	NSGLLQDEPT	VKtFNAMNVE	YGTIGNHEFD EGLAEYNRIV TGKAPAPDSN
msa237615.2{328_M732}	NSGLLQDEPT	VKtFNAMNVE	YGTIGNHEFD EGLAEYNRIV TGKAPAPDSN
msa237615.2{328_COH1}	NSGLLQDEPT	VKtFNAMNVE	YGTIGNHEFD EGLAEYNRIV TGKAPAPDSN
msa237615.2{328_M781}	NSGLLQDEPT	VKtFNAMNVE	YGTIGNHEFD EGLAEYNRIV TGKAPAPDSN
msa237615.2{328_H36B}	NSGLLQDEPT	VKtFNAMNVE	YGTIGNHEFD EGLAEYNRIV TGKAPAPDSN
msa237615.2{328_JM9130013}	NSGLLQDEPT	VKtFNAMNVE	YGTIGNHEFD EGLAEYNRIV TGKAPAPDSN
msa237615.2{328_18RS21}	NSGLLQDEPT	VKtFNAMNVE	YGTIGNHEFD EGLAEYNRIV TGKAPAPDSN
msa237615.2{328_090}	NSGLLQDEPT	VKtFNAMNVE	YGTIGNHEFD EGLAEYNRIV TGKAPAPDSN
msa237615.2{328_CJB110}	NSGLLQDEPT	VKtFNAMNVE	YGTIGNHEFD EGLAEYNRIV TGKAPAPDSN
Consensus	*****	*****	*****
	151		200
msa237615.2{328_1169NT}	INNITKSYPH	EAAKQEIIVA	NVIDKVNKQI PYNWKPYaIK NIPVNNKSVN
msa237615.2{328_2603}	INNITKSYPH	EAAKQEIIVA	NVIDKVNKQI PYNWKPYaIK NIPVNNKSVN
msa237615.2{328_A909}	INNITKSYPH	EAAKQEIIVA	NVIDKVNKQI PYNWKPYtIK NIPVNNKSVN
msa237615.2{328_M732}	INNITKSYPH	EAAKQEIIVA	NVIDKVNKQI PYNWKPYtIK NIPVNNKSVN
msa237615.2{328_COH1}	INNITKSYPH	EAAKQEIIVA	NVIDKVNKQI PYNWKPYtIK NIPVNNKSVN
msa237615.2{328_M781}	INNITKSYPH	EAAKQEIIVA	NVIDKVNKQI PYNWKPYtIK NIPVNNKSVN

Table 71: Comparative Sequences relating to SAG1333

msa237615.2{328_H36B}	INNITKSYPH	EAAKQEI VVA	NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN
msa237615.2{328_JM9130013}	INNITKSYPH	EAAKQEI VVA	NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN
msa237615.2{328_18RS21}	INNITKSYPH	EAAKQEI VVA	NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN
msa237615.2{328_090}	INNITKSYPH	EAAKQEI VVA	NVIDKVNKQI	PYNWKPYaIK	NIPVNNKSVN
msa237615.2{328_CJB110}	INNITKSYPH	EAAKQEI VVA	NVIDKVNKQI	PYNWKPYaIK	NIPVNNKSVN
Consensus	*****	*****	*****	*****_*	*****
201					
msa237615.2{328_1169NT}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLDEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_2603}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLDEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_A909}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLDEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_M732}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLDEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_COH1}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLDEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_M781}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLDEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_H36B}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLDEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_JM9130013}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLDEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_18RS21}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLDEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_090}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLDEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_CJB110}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLDEAE	TIVKYAKELQ	AKNVKAI VVL
Consensus	*****	*****	*****	*****	*****
251					
msa237615.2{328_1169NT}	AHV PATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_2603}	AHV PATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_A909}	AHV PATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_M732}	AHV PATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_COH1}	AHV PATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_M781}	AHV PATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_H36B}	AHV PATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_JM9130013}	AHV PATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_18RS21}	AHV PATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_090}	AHV PATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_CJB110}	AHV PATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
Consensus	*****_*	*****	*****	*****	*****
301					
msa237615.2{328_1169NT}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_2603}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_A909}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_M732}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_COH1}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_M781}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_H36B}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_JM9130013}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_18RS21}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_090}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_CJB110}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
Consensus	*****	*****	*****	*****_****	*****
351					
msa237615.2{328_1169NT}	AIVDQANTIV	KQVTEAKIGT	AEVSvMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_2603}	AIVDQANTIV	KQVTEAKIGT	AEVSvMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_A909}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_M732}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_COH1}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_M781}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_H36B}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_JM9130013}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_18RS21}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_090}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_CJB110}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
Consensus	*****	*****	*****_*****	*****	*****
401					
msa237615.2{328_1169NT}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_2603}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_A909}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_M732}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_COH1}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_M781}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_H36B}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_JM9130013}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_18RS21}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_090}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_CJB110}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
Consensus	*****	*****	*****	*****	*****
451					
msa237615.2{328_1169NT}	TGRDLYKALN	EQYDQKQNF	LQIAGLRITY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_2603}	TGRDLYKALN	EQYDQKQNF	LQIAGLRITY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_A909}	TGRDLYKALN	EQYDQKQNF	LQIAGLRITY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_M732}	TGRDLYKALN	EQYDQKQNF	LQIAGLRITY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_COH1}	TGRDLYKALN	EQYDQKQNF	LQIAGLRITY	TDNKEGGEET	PFKVVKAYKS

Table 71: Comparative Sequences relating to SAG1333

msa237615.2{328_M781}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_H36B}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_JM9130013}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_18RS21}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_090}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_CJB110}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
Consensus	*****	*****	*****	*****	*****
msa237615.2{328_1169NT}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_2603}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_A909}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_M732}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_COH1}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_M781}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_H36B}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_JM9130013}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_18RS21}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_090}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_CJB110}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
Consensus	*****	*****	*****	*****	*****
msa237615.2{328_1169NT}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi
msa237615.2{328_2603}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi
msa237615.2{328_A909}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi
msa237615.2{328_M732}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi
msa237615.2{328_COH1}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi
msa237615.2{328_M781}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi
msa237615.2{328_H36B}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi
msa237615.2{328_JM9130013}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi
msa237615.2{328_18RS21}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi
msa237615.2{328_090}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi
msa237615.2{328_CJB110}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi
Consensus	*****	*****	*****	*****	*****
msa237615.2{328_1169NT}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_2603}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_A909}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_M732}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_COH1}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_M781}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_H36B}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_JM9130013}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_18RS21}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_090}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_CJB110}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
Consensus	*****	*****	*****	*****	*****
msa237615.2{328_1169NT}	TVKS-----	-----	-----	-----	690
msa237615.2{328_2603}	TVKSKQlpkt	nseyggsflm	svfgvgligi	alntkckhmk	
msa237615.2{328_A909}	TVKSKQ----	-----	-----	-----	
msa237615.2{328_M732}	TVKSKQ----	-----	-----	-----	
msa237615.2{328_COH1}	TVKS-----	-----	-----	-----	
msa237615.2{328_M781}	TVKS-----	-----	-----	-----	
msa237615.2{328_H36B}	TVKS-----	-----	-----	-----	
msa237615.2{328_JM9130013}	TVKSK-----	-----	-----	-----	
msa237615.2{328_18RS21}	TVKSK-----	-----	-----	-----	
msa237615.2{328_090}	TVKSKQ----	-----	-----	-----	
msa237615.2{328_CJB110}	TVKS-----	-----	-----	-----	
Consensus	*****	*****	*****	*****	

Table 72: Comparative Sequences relating to SAG0941

SEQ ID NO. 7201

STRAIN 2603

ATGAATAAACGCGTAAAAATCGTTGCAACACTTGGTCCCTGCGGTTGAATTCGGTGGTG
 GTAAGAAGTTTGGTGAGTCTGGGATCTGGGTTGAAAGCCTTGACGTAGAAGCTTCAGCAG
 AAAAAATTGCTCAATTGATTAAAGAAGGTGCTAACGTTTCCGTTTCAACTTCTCACATG
 GAGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAGAGATTGCAG
 GACAAAAAGTTGGCTTCCCTCTTGATACTAAAGGACCTGAAATTCGTACAGAAGCTTTTGG
 AAGATGGTGACAGATTTCCATTCAATATACAACAGGTACAAAAATTACGTGTTGCTACTAAGC
 AAGGTATCAAATCACTCCAGAAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCT
 TTGATGACGTTGAAGTTGGTAAGCAAATCCTTGTGATGATGGTAACTAGGTCTTACTG
 TGTTTGC AAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATGATGGCCCTTA
 TTGGTAAACAAAAGGTGTAACATCCCTTATACTAAATTCCTTTCCAGCACTTGCGAG
 AACGCGATAATGCTGATATCCGTTTGGACTTGAGCAAGGACTTAACCTTATTGCTATCT
 CATTTGTACGTACTGCTAAAAGATGTTAATGAAGTTCGTGCTATTTGTGAAGAACTGGsm
 ATGGACACGTTAAGTTGTTTCTAAAATTTGAAATCAACAAGGTATCGATAATATTGATG
 AGATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTATCGAAGTTC
 CATTTGAAATGTTCCAGTTTACCAAAAAATGATCATTAATAAGTTAATGCAGCTGGTA
 AAGCAGTTATTACAGCAACAAATATGCTTGAACAATGACTGATAAACCCAGTGCAGCTC
 GTTCAGAAGTATCTGATGCTTCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTT
 CAGGTGAGTCAGCTAATGGTAAATACCCAGTTGAGTCAGTTGTAACATGGCTACTATTG
 ATAAAAATGCTCAAACATTACTCAATGAGTATGGTGGCTTAGACTGCTGCAATCCAC
 GTAATAACAAAATCATGTTATTGCTATCTGCGGTTAAAGATGCAACACACTCAATGGATA
 TCAAACTTGTGTTAAACAATTAAGTAAACAGGTAAATACAGCTCGTGCCATTTCTAAATCC
 GTCCAGATGCAACACTTTGGCTGTTACATTTGATGAAAAAGTACAAAGCTTCATTGATGA
 TTAAGTGGGGTGTATCCCTGCTCTGACAGCAAAACAGCATCTACAGATGATATGTTG
 AGGTTGCAGAAGCTGTAGCACTTGAAGCAGGATTGTTGAATCAGGCGATAATATCGTTA
 TCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACAAACAATGCGTGTTCGTACTGTTA
 AA

SEQ ID NO. 7202

STRAIN 090

AATAAACGCGTAAAAATCGTTGCAACACT
 TGGTCCCTGCGGTAGAATTCGGTGGTGAAGAAGTTTGGTGAGTCTGGAT
 ACTGGGGTGAAGCCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCTCAA
 TTGATTAAAGAAGGTGCTAACGTTTCCGTTTCAACTTCTCACATGGAGA
 TCAATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAGAGA
 TTGCAGGACAAAAAGTTGGCTTCCCTCTTGATACTAAAGGACCTGAAAT
 CGTACAGAACTTTTGAAGATGGTTGAGATTCCATTCAATATACAACAGG
 TACAGAATTACGTGTTGCTACTAAGCAAGGTATCAATCAACTCCAGAAG
 TGATTGCAATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTTGAA
 GTTGGTAAAGCAATCCTTGTGATGATGGTAAACTAGGTCTTACTGTGTT
 TGCAAAAGATAAAGCACTCGTGAATTTGAAGTAGTTGTTGAGAATGATG
 GCCTTATTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAATTCCT
 TTCCCAgCACTTGCAAGCGGATTAATGCTGATCCGTTTGGACTTGA
 GCAAGGACTTAACCTTTATTGCTATCTCATTGTGACGTACTGCTAAAGATG
 TTAATGAAGTTCGTGCTATTGTTGAAGAACTGGCAATGGACATGTTAAG
 TTGTTTGTCTAAATTTGAAATCAACAAGGTATCGATAATATTGATGAGAT
 TATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTATCG
 AAGTTCCTATTGAAATGGTTCCAGTTTACCAAAAAATGATCACTACTAAA
 GTTAATGCACTGGTAAAGCAGTTATTACAGCAACAATATGCTTGAAC
 AATGACTGATAAACCAGCTGCGACTCGTTCAGAAGTATCTGATGCTTCA
 ATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCAGCT
 AATGGTAAATACCCAGTTGAGTCAGTTGCTACAATGGCTACTATTGATAA
 AATGCTCAAACTTACTCAATGAGTATGGTGGCTTAGACTCATCTGCAT
 TCCCACTAATAACAAAATGATGTTATTGCTATCTGCGGTTAAAGATGCA
 ACACACTCAATGGATATCAAACTTGTGTGACAATTACTGAAACAGGTAA
 TACAGCTCGTGCCATTCTAAATTCGTCAGATGACAGATTTTGGCTG
 TTACATTTGATGAAAAAGTACAACGTTTATTGATGATTAACTGGGGTGT
 ATCCCTGTCTTGCAGACAAACAGCATCTACAGATGATATGTTTGAAGT
 TGCAGAAGCTGTAGCACTTGAAGCAGGACTTGTGAATCAGGCGATAATA
 TCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACAAACAATG
 CGTGTTCGTACTGTTAAA

SEQ ID NO. 7203

STRAIN A909

AATAAACGCGTAAAAATCGTTGCAACACTTGGTC
 CTGCGGTTGAATTCGGTGGTGAAGAAGTTTGGTGAGTCTGGGATCTGG
 GGTGAAGCCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCTCAATTGAT
 TAAAGAAGGTGCTAACGTTTCCGTTTCAACTTCTCACATGGAGATCATG
 CTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAGAGATTGCA
 GGACAAAAAGTTGGCTTCCCTCTTGATACTAAAGGACCTGAAATTCGTAC
 AGAAGCTTTTGAAGATGGTGAGATTTCATTCAATATACAACAGGTACAA
 AATTACGTTGTTGCTACTAAGCAAGGTATCAATCAACTCCAGAAGTGATT
 GCAATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTTGAAGTTGG
 TAAGCAAACTCCTTGTGATGATGGTAACTAGGTCTTACTGTGTTTGC
 AAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATGATGGCTT
 ATTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAAATTCCTTTCC
 AGCACTTGCAAGACGCGATAATGCTGATATCCGTTTGGACTTGAGCAAG
 GACTTAACCTTTATTGCTATCTCATTGTGACGTACTGCTAAAGATGTTAAT
 GAAGTTCTGCTATTGTTGAAGAACTGGCAATGGACAGCTTAAGTTGTT
 TGCTAAAAATTTGAAATCAACAAGGTATCGATAATATTGATGAGATTATCG
 AAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTATCGAAGTT
 CCATTGAAATGTTCCAGTTTACCAAAAAATGATCATTAATAAGTTAA

Table 72: Comparative Sequences relating to SAG0941

TGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGAAACAATGA
CTGATAAACCCAGTCGCGACTCGTTTCAGAGATCTGATGTCTTCAATGCT
GTTATTGATGGTACTGATGCTACAATGCTTTTCAGGTGAGTCAGCTAATGG
TAAATACCCAGTTGAGTCAGTTTCGTACATGGCTACTATTGATAAAAATG
CTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTGCATTCCCA
CGTAATAACAAAACTGATGTTATTGCACTCGCGTTAAAGATGCAACACA
CTCAATGGATATCAAACTTGTGTAAACAATTACTGAAACAGGTAATACAG
CTCGTGCCATTCTTAAATTCGGTCCAGATGCAGACATTTTGGCTGTTACA
TTTGATGAAAAAGTACAACGTTTCATTGATGATTAACITGGGGTGTATCCC
TGCTCTGTCAGACAAACCAGCATCTACAGATGATATGTTTGGAGTTGCGAG
AACGTGTAGCACTTGAAGCAGGATTGTTGAATCAGGCGATAATATCGTT
ATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACCTAACCAATGCGGTG
TCGTACTGTTAAA

SEQ ID NO. 7204

STRAIN H36B

AATAAACCGGTAAAAATCGTTGCAAC
ACTTGGTCTCGCGTTGAATTCGGTGGTGAAGTTTGGTGAGTCTG
GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATGCT
CAATTGATTAAAGAAGGTGCTAACGTTTCCGTTTCAACTTCTCATATGG
AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTCTGTAAGCAGAAG
AGATTGCAAGGACAAAAAGTTGGCTTCTCTTGATACTAAAGGACCTGAA
ATTTCGTACAGAACTTTTGAAGATGGTGCAAGTTTCCATTATATACAAC
AGGTACAAAAATTACGTGTTGCTACTAAGCAAGGTATCAAAATCAACTCCAG
AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
GAAGTTGGTAAGCAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
GTTTGCAAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
ATGGCCTTATTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAAAT
CCTTTCAGCACTTGCAGAACCGGATAATGCTGATATCCGTTTGGACT
TGAGCAAGGACTTAACCTTTATTGCTATCTCATTGTGACGTACTGCTAAAG
ATGTTAATGAAGTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
AAGTTGTTTGTCTAAAAATGAAAAATCAACAAGGTATCGATAATATTGATGA
GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
TCGAAGTTCCATTGAAATGGTTCAGTTTACCAAAAAATGATCAITACT
AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
AACCAATGACTGATAAACCAAGTGGCGACTCGTTGAGAAGTATCTGATGTCT
TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
GCTAATGGTAAATACCCAGTTGAGTCAGTTCTGATCAATGGCTACTATTGA
TAAAAATGCTCAAACTTACTCAATGAGTATGGTCGCTTAGACTCATCTG
CAITCCCACGTAATAACAAACTGATGTTATTGCACTCGCGGTTAAAGAT
GCAACACACTCAATGGATATCAAACTTGTGTAAACAATTACTGAAACAGG
TAATACAGCTCGTGCCATTCTTAAATTCGGTCCAGATGCAGACATTTTGG
CTGTTACATTGATGAAAAAGTACAACGTTTCATTGATGATTAACITGGGGT
GTTATCCCTGTCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGA
GGTTGCAGAACGTGTAGCACTTGAAGCAGGATTGTTGAATCAGGCGATA
ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACCTAACACA
ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7205

STRAIN 18RS21

AATAAACCGGTAAAAATCGTTGCAAC
ACTTGGTCTCGCGTTGAATTCGGTGGTGAAGTTTGGTGAGTCTG
GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATGCT
CAATTGATTAAAGAAGGTGCTAACGTTTCCGTTTCAACTTCTCATATGG
AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTCTGTAAGCAGAAG
AGATTGCAAGGACAAAAAGTTGGCTTCTCTTGATACTAAAGGACCTGAA
ATTTCGTACAGAACTTTTGAAGATGGTGCAAGTTTCCATTATATACAAC
AGGTACAAAAATTACGTGTTGCTACTAAGCAAGGTATCAAAATCAACTCCAG
AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
GAAGTTGGTAAGCAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
GTTTGCAAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
ATGGCCTTATTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAAAT
CCTTTCAGCACTTGCAGAACCGGATAATGCTGATATCCGTTTGGACT
TGAGCAAGGACTTAACCTTTATTGCTATCTCATTGTGACGTACTGCTAAAG
ATGTTAATGAAGTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
AAGTTGTTTGTCTAAAAATGAAAAATCAACAAGGTATCGATAATATTGATGA
GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
TCGAAGTTCCATTGAAATGGTTCAGTTTACCAAAAAATGATCAITACT
AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
AACCAATGACTGATAAACCAAGTGGCGACTCGTTGAGAAGTATCTGATGTCT
TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
GCTAATGGTAAATACCCAGTTGAGTCAGTTCTGATCAATGGCTACTATTGA
TAAAAATGCTCAAACTTACTCAATGAGTATGGTCGCTTAGACTCATCTG
CAITCCCACGTAATAACAAACTGATGTTATTGCACTCGCGGTTAAAGAT
GCAACACACTCAATGGATATCAAACTTGTGTAAACAATTACTGAAACAGG
TAATACAGCTCGTGCCATTCTTAAATTCGGTCCAGATGCAGACATTTTGG
CTGTTACATTGATGAAAAAGTACAACGTTTCATTGATGATTAACITGGGGT
GTTATCCCTGTCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGA
GGTTGCAGAACGTGTAGCACTTGAAGCAGGATTGTTGAATCAGGCGATA
ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACCTAACACA
ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7206

Table 72: Comparative Sequences relating to SAG0941

STRAIN M732

AATAAACGCGTAAAAATCGTTGCAAC
 ACTTGGTCCTGCGGTAGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTGTAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATATAAAGGACCTGAA
 ATTGCTACAGAACTTTTGAAGATGGTGCAGATTCCATTATATACAAC
 AGGTACAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAAAT
 CCTTTCCAGCACTTGCGAAGCGGATAATGCTGATATCCGTTTTGGACT
 TGAGCAAGGACTTAACTTTATGCTATCTCATTGTGACGTACTGCTAAAG
 ATGTTAATGAAGTTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTTGCTAAAAATTGAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCCATTGAAATGGTTCAGTTTACCAAAAAATGATCATTACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGACTGATAAACCCAGTGCAGCTCGTTGAGAAGTATCTGATGTCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTGCTACAAATGGCTACTATTGA
 TAAAAATGCTCAAACTTACTCAATGAGTATGGTTCGCTTAGACTCATCTG
 CATTTCCACGTAATAACAAACTGATGTTATTGCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAATTTGTTGTAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAATTCGGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTTCAATGATGATTAACTGGGGT
 GTTATCCCTGTCTTGCAGACAAACAGCATCTACAGATGATATGTTTGA
 GGTTCAGAACGTTGACACTTGAAGCAGGACTTGTGTAATCAGGCGATA
 ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACATAACACA
 ATGCGTGTTCGTACTGTTAA

SEQ ID NO. 7207

STRAIN COH1

AATAAACGCGTAAAAATCGTTGCAAC
 ACTTGGTCCTGCGGTAGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTGTAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATATAAAGGACCTGAA
 ATTGCTACAGAACTTTTGAAGATGGTGCAGATTCCATTATATACAAC
 AGGTACAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGTTAAACAAAAAGGTGTAACATCCCTTATACTAAAAAT
 CCTTTCCAGCACTTGCGAAGCGGATAATGCTGATATCCGTTTTGGACT
 TGAGCAAGGACTTAACTTTATGCTATCTCATTGTGACGTACTGCTAAAG
 ATGTTAATGAAGTTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTTGCTAAAAATTGAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCCATTGAAATGGTTCAGTTTACCAAAAAATGATCATTACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGCTGATAAACCCAGTGCAGCTCGTTGAGAAGTATCTGATGTCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTGCTACAAATGGCTACTATTGA
 TAAAAATGCTCAAACTTACTCAATGAGTATGGTTCGCTTAGACTCATCTG
 CATTTCCACGTAATAACAAACTGATGTTATTGCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAATTTGTTGTAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAATTCGGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTTCAATGATGATTAACTGGGGT
 GTTATCCCTGTCTTGCAGACAAACAGCATCTACAGATGATATGTTTGA
 GGTTCAGAACGTTGACACTTGAAGCAGGACTTGTGTAATCAGGCGATA
 ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACATAACACA
 ATGCGTGTTCGTACTGTTAA

SEQ ID NO. 7208

STRAIN M781

AATAAACGCGTAAAAATCGTTGCAAC
 ACTTGGTCCTGCGGTAGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTGTAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATATAAAGGACCTGAA
 ATTGCTACAGAACTTTTGAAGATGGTGCAGATTCCATTATATACAAC
 AGGTACAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGTTAAACAAAAAGGTGTAACATCCCTTATACTAAAAAT
 CCTTTCCAGCACTTGCGAAGCGGATAATGCTGATATCCGTTTTGGACT
 TGAGCAAGGACTTAACTTTATGCTATCTCATTGTGACGTACTGCTAAAG

Table 72: Comparative Sequences relating to SAG0941

ATGTTAATGAAGTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTTGTCTAAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCATTGAAATGGTTCAGTTTACCAAAAAATGATCATTA
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGACTGATAAACACCGTGGCTCGTTTCTGAGTATCTGATGCT
 TCAATGCTGTTTATGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTTCTGACAATGGCTACTATTGA
 TAAAAATGCTCAAACTTACTCAATGAGTATGGTTCGCTTAGACTCATCTG
 CATTTCCACGTAATAACAAACTGATGTTATTGTCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACTTGTGTGAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAGTTCGGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTCAITGATGATTAACTGGGGT
 GTTATCCCTGTCCTTGAGACAAACAGCATCTACAGATGATATGTTTGA
 GGTTCAGAACGTTGACACTTGAAGCAGGACTTGTGAATCAGGCGATA
 ATATCGTTATCGTTGAGGTGTTCTGTAGGTACAGGTGGAACATAACACA
 ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7209

STRAIN CJB110

AATAAACCGGTAAAAATCGTTGCAAC
 ACTTGGTCTCGCGTTGAATTCGGTGGTGAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTTGATTAAAGAAGGTGCTAACGTTTTCGGTTTCAACTTCTCATATGG
 AGATCATGCTGAGCAAGCAGCTCGTATGGCTACTGTTTCTGTAAGCAGAAG
 AGATTGACAGGACAAAAAGTTGGCTTCTCTTGTATCTAAAGGACCTGAA
 ATTCTGACAGAACTTTTGAAGATGGTGCAGATTTCATTCATATACAAC
 AGGTACAAAATTACGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCAATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAATT
 CCTTTCCAGCACTTGAGAACGCGATAATGCTGATATCCGTTTGGACT
 TGAACAAGGACTTAACCTTTATTGCTATCTCATTTGTACGTACTGCTAAAG
 ATGTTAATGAAGTTTCTGCTATTTGTGAAGAACTGGCAATGGACAGTT
 AAGTTGTTTGTCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCATTGAAATGGTTCAGTTTACCAAAAAATGATCATTA
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGACTGATAAACACCGTGGCTCGTTTCTGAGTATCTGATGCT
 TCAATGCTGTTTATGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTTCTGACAATGGCTACTATTGA
 TAAAAATGCTCAAACTTACTCAATGAGTATGGTTCGCTTAGACTCATCTG
 CATTTCCACGTAATAACAAACTGATGTTATTGTCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACTTGTGTGAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAATTCGGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTCAITGATGATTAACTGGGGT
 GTTATCCCTGTCCTTGAGACAAACAGCATCTACAGATGATATGTTTGA
 GGTTCAGAACGTTGACACTTGAAGCAGGATTGTTGAATCAGGCGATA
 ATATCGTATATCGTTGAGGTGTTCTGTAGGTACAGGTGGAACATAACACA
 ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7210

STRAIN 1169NT

AATAAACCGGTAAAAATCGTTGCAAC
 ACTTGGTCTCGCGTGAATTCGGTGGTGAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTTGATTAAAGAAGGTGCTAACGTTTTCGGTTTCAACTTCTCATATGG
 AGATCATGCTGAGCAAGCAGCTCGTATGGCTACTGTTTCTGTAAGCAGAAG
 AGATTGACAGGACAAAAAGTTGGCTTCTCTTGTATCTAAAGGACCTGAA
 ATTCTGACAGAACTTTTGAAGATGGTGCAGATTTCATTCATATACAAC
 AGGTACAAAATTACGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCAATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAATT
 CCTTTCCAGCACTTGAGAACGCGATAATGCTGATATCCGTTTGGACT
 TGAGCAAGGACTTAACCTTTATTGCTATCTCATTTGTACGTACTGCTAAAG
 ATGTTAATGAAGTTTCTGCTATTTGTGAAGAACTGGCAATGGACAGTT
 AAGTTGTTTGTCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCATTGAAATGGTTCAGTTTACCAAAAAATGATCATTA
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGACTGATAAACACCGTGGCTCGTTTCTGAGTATCTGATGCT
 TCAATGCTGTTTATGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTTCTGACAATGGCTACTATTGA
 TAAAAATGCTCAAACTTACTCAATGAGTATGGTTCGCTTAGACTCATCTG
 CATTTCCACGTAATAACAAACTGATGTTATTGTCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACTTGTGTGAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAATTCGGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTCAITGATGATTAACTGGGGT
 GTTATCCCTGTCCTTGAGACAAACAGCATCTACAGATGATATGTTTGA
 GGTTCAGAACGTTGACACTTGAAGCAGGATTGTTGAATCAGGCGATA
 ATATCGTATATCGTTGAGGTGTTCTGTAGGTACAGGTGGAACATAACACA
 ATGCGTGTTCGTACTGTTAAA

Table 72: Comparative Sequences relating to SAG0941

ATATCGTTATCGTTGCAGGTGTTCTCTGTAGGTACAGGTGGAACCTAACACA
ATGCGTGTTCGTACTGTTAA

SEQ ID NO. 7211

STRAIN JM9130013

AATAAACCGGTAAAAATCGTTGCAAC

ACTTGGTCCCTGCGGTAGAAATCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
GATACCTGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
CAATTGATTAAAGAAGGTGCTAACGTTTCCGTTCACACTTCTCACATGG
AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTCTGTAAGCAGAAG
AGATTGCAGGACAAAAAGTTGGCTTCTCTCTGATACTAAAGGACCTGAA
ATTCGTACAGAACTTTTGAAGATGGTTCAGATTTCCATTTCATATACAAC
AGGTACAAAATTACGTGTTGCTACTAAGCAAGGTATCAATCAACTCCAG
AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
GAAGTTGGTAAGCAAAATCCTTGTGTGATGATGGTAACTAGGTCTTACTGT
GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
ATGGCCTTATTTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAAAT
CCTTTCCAGCACTTGCAGAACGCGATAATGCTGATATCCGTTTGGACT
TGAGCAAGGACTTAACCTTTATTGCTATCTCATTTGTACGTACTGCTAAAG
ATGTTAATGAAGTTTCTGCTATTGTGTAAGAACTGGCAATGGACATGTT
AAGTTGTTTGTCTAAAATTGAATAACAAGGTATCGATAAATATTGATGA
GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
TCGAAGTTCCATTTGAAATGGTTCCAGTTTACCAAAAAATGATCATTACT
AAAGTTAATGCAAGCTGGTAAAGCAGTTATACAGCAACAATATGCTTGA
AACAAATGACTGATAAACCCAGTGCAGCTCGTTTCAAGATATCTGATGCT
TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
GCTAATGGTAAATACCCAGTTGAGTCACTTTCGTACAATGGCTACTATTGA
TAAAAATGCTCAACATTACTCAATGAGTATGGTTCGCTTAGACTCATCTG
CATTTCCAGCTAATAACAAAACTGATGTTATGCACTGCGGTTAAAGAT
GCACACACTCAATGGATATCAAACTGTTGTGACAATTACTGAAACAGG
TAATACAGCTCGTGCCATTTCTAAATCCGTCCAGATGCAGACATTTTGG
CTGTTACATTTGATGAAAAAGTACAACGTTTATTGATGATTAACTGGGT
GTATCCCTGTCCTTGCAGACAAACAGCATCTACAGATGATATGTTTGA
GGTTGCAGAACGTGTAGcACTTGAAGCAGGACTTGTGAATCAGGCGATA
ATATCGTTATCGTTGCAGGTGTTCTCTGTAGGTACAGGTGGAACCTAACACA
ATGCGTGTTCGTACTGTTAA

PRETTY of: /biotmp/msa277466.2{*} February 24, 2003 01:44 ..

	1		50
msa277466.2{330_090}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_JM9130013}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_18RS21}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_2603}	atgAATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_A909}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_H36B}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_CJB110}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_COH1}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_M732}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_1169NT}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_M781}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
Consensus	*****	*****	*****
	51		100
msa277466.2{330_090}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_JM9130013}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_18RS21}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_2603}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_A909}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_H36B}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_CJB110}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_COH1}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_M732}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_1169NT}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_M781}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
Consensus	*****	*****	*****
	101		150
msa277466.2{330_090}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_JM9130013}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_18RS21}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_2603}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_A909}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_H36B}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_CJB110}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_COH1}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_M732}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_1169NT}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_M781}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
Consensus	*****	*****	*****
	151		200
msa277466.2{330_090}	AACGTTTTTC	GTTTCAACTT	CTCACATGGA

Table 72: Comparative Sequences relating to SAG0941

msa277466.2{330_JM9130013}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_18RS21}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_2603}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_A909}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_H36B}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_CJB110}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_COH1}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_M732}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_1169NT}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_M781}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_JM9130013}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_18RS21}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_2603}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_A909}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_H36B}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_CJB110}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_COH1}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_M732}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_1169NT}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_M781}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTGTAA
msa277466.2{330_JM9130013}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTGTAA
msa277466.2{330_18RS21}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTGTAA
msa277466.2{330_2603}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTGTAA
msa277466.2{330_A909}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTGTAA
msa277466.2{330_H36B}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTGTAA
msa277466.2{330_CJB110}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTGTAA
msa277466.2{330_COH1}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTGTAA
msa277466.2{330_M732}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTGTAA
msa277466.2{330_1169NT}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTGTAA
msa277466.2{330_M781}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTGTAA
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	GATGGTtCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_JM9130013}	GATGGTtCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_18RS21}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_2603}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_A909}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_H36B}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_CJB110}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_COH1}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_M732}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_1169NT}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_M781}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
Consensus	*****_***	*****	*****	*****_***	*****
msa277466.2{330_090}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_JM9130013}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_18RS21}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_2603}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_A909}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_H36B}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_CJB110}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_COH1}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_M732}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_1169NT}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_M781}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_JM9130013}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_18RS21}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_2603}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_A909}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_H36B}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_CJB110}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_COH1}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_M732}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_1169NT}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_M781}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
Consensus	*****	*****	*****	*****	*****

451

500

Table 72: Comparative Sequences relating to SAG0941

msa277466.2{330_090}	GTTGATGATG	GTAAGCTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_JM9130013}	GTTGATGATG	GTAAGCTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_18RS21}	GTTGATGATG	GTAAGCTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_2603}	GTTGATGATG	GTAAGCTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_A909}	GTTGATGATG	GTAAGCTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_H36B}	GTTGATGATG	GTAAGCTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_CJB110}	GTTGATGATG	GTAAGCTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_COH1}	GTTGATGATG	GTAAGCTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_M732}	GTTGATGATG	GTAAGCTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_1169NT}	GTTGATGATG	GTAAGCTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_M781}	GTTGATGATG	GTAAGCTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_JM9130013}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_18RS21}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_2603}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_A909}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_H36B}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_CJB110}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_COH1}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_M732}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_1169NT}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_M781}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACGAG	ACTTGCAGAA
msa277466.2{330_JM9130013}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACGAG	ACTTGCAGAA
msa277466.2{330_18RS21}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACGAG	ACTTGCAGAA
msa277466.2{330_2603}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACGAG	ACTTGCAGAA
msa277466.2{330_A909}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACGAG	ACTTGCAGAA
msa277466.2{330_H36B}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACGAG	ACTTGCAGAA
msa277466.2{330_CJB110}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACGAG	ACTTGCAGAA
msa277466.2{330_COH1}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACGAG	ACTTGCAGAA
msa277466.2{330_M732}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACGAG	ACTTGCAGAA
msa277466.2{330_1169NT}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACGAG	ACTTGCAGAA
msa277466.2{330_M781}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACGAG	ACTTGCAGAA
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_JM9130013}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_18RS21}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_2603}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_A909}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_H36B}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_CJB110}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_COH1}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_M732}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_1169NT}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_M781}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_JM9130013}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_18RS21}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_2603}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_A909}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_H36B}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_CJB110}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_COH1}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_M732}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_1169NT}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_M781}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	TTTGTGAAGA	AACCTGGcaAT	GGACAcGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_JM9130013}	TTTGTGAAGA	AACCTGGcaAT	GGACAcGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_18RS21}	TTTGTGAAGA	AACCTGGcaAT	GGACAcGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_2603}	TTTGTGAAGA	AACCTGGsmAT	GGACAcGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_A909}	TTTGTGAAGA	AACCTGGcaAT	GGACAcGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_H36B}	TTTGTGAAGA	AACCTGGcaAT	GGACAcGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_CJB110}	TTTGTGAAGA	AACCTGGcaAT	GGACAcGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_COH1}	TTTGTGAAGA	AACCTGGcaAT	GGACAcGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_M732}	TTTGTGAAGA	AACCTGGcaAT	GGACAcGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_1169NT}	TTTGTGAAGA	AACCTGGcaAT	GGACAcGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_M781}	TTTGTGAAGA	AACCTGGcaAT	GGACAcGTTA	AGTTGTTTGC	TAAAATTGAA
Consensus	*****	*****	*****	*****	*****

Table 72: Comparative Sequences relating to SAG0941

		751					800
msa277466.2{330_090}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_JM9130013}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_18RS21}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_2603}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_A909}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_H36B}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_CJB110}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_COH1}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_M732}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_1169NT}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_M781}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
Consensus	*****	*****	*****	*****	*****		
		801					850
msa277466.2{330_090}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_JM9130013}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_18RS21}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_2603}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_A909}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_H36B}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_CJB110}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_COH1}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_M732}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_1169NT}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_M781}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
Consensus	*****	*****	*****	*****	*****		
		851					900
msa277466.2{330_090}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_JM9130013}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_18RS21}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_2603}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_A909}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_H36B}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_CJB110}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_COH1}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_M732}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_1169NT}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_M781}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
Consensus	*****	*****	*****	*****	*****		
		901					950
msa277466.2{330_090}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_JM9130013}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_18RS21}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_2603}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_A909}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_H36B}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_CJB110}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_COH1}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_M732}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_1169NT}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_M781}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
Consensus	*****	*****	*****	*****	*****		
		951					1000
msa277466.2{330_090}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_JM9130013}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_18RS21}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_2603}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_A909}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_H36B}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_CJB110}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_COH1}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_M732}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_1169NT}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_M781}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
Consensus	*****	*****	*****	*****	*****		
		1001					1050
msa277466.2{330_090}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_JM9130013}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_18RS21}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_2603}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_A909}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_H36B}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_CJB110}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_COH1}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_M732}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_1169NT}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_M781}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
Consensus	*****	*****	*****	*****	*****		

Table 72: Comparative Sequences relating to SAG0941

		1051			1100
msa277466.2{330_090}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_JM9130013}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_18RS21}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_2603}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_A909}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_H36B}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_CJB110}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_COH1}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_M732}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_1169NT}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_M781}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
Consensus		*****	*****	*****	*****
		1101			1150
msa277466.2{330_090}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_JM9130013}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_18RS21}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_2603}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_A909}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_H36B}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_CJB110}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_COH1}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_M732}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_1169NT}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_M781}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
Consensus		*****	*****	*****	*****
		1151			1200
msa277466.2{330_090}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_JM9130013}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_18RS21}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_2603}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_A909}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_H36B}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_CJB110}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_COH1}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_M732}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_1169NT}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_M781}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
Consensus		*****	*****	*****	*****
		1201			1250
msa277466.2{330_090}		AAACTTGTTG	TgACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_JM9130013}		AAACTTGTTG	TgACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_18RS21}		AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_2603}		AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_A909}		AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_H36B}		AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_CJB110}		AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_COH1}		AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_M732}		AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_1169NT}		AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_M781}		AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
Consensus		*****	*****	*****	*****
		1251			1300
msa277466.2{330_090}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_JM9130013}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_18RS21}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_2603}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_A909}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_H36B}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_CJB110}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_COH1}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_M732}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_1169NT}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_M781}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
Consensus		***-*****	*****	*****	*****
		1301			1350
msa277466.2{330_090}		TACAACGTTT	ATTGATGATT	AAC TG GGGTG	TTATCCCTGT
msa277466.2{330_JM9130013}		TACAACGTTT	ATTGATGATT	AAC TG GGGTG	TTATCCCTGT
msa277466.2{330_18RS21}		TACAACGTTT	ATTGATGATT	AAC TG GGGTG	TTATCCCTGT
msa277466.2{330_2603}		TACAACGTTT	ATTGATGATT	AAC TG GGGTG	TTATCCCTGT
msa277466.2{330_A909}		TACAACGTTT	ATTGATGATT	AAC TG GGGTG	TTATCCCTGT
msa277466.2{330_H36B}		TACAACGTTT	ATTGATGATT	AAC TG GGGTG	TTATCCCTGT
msa277466.2{330_CJB110}		TACAACGTTT	ATTGATGATT	AAC TG GGGTG	TTATCCCTGT
msa277466.2{330_COH1}		TACAACGTTT	ATTGATGATT	AAC TG GGGTG	TTATCCCTGT
msa277466.2{330_M732}		TACAACGTTT	ATTGATGATT	AAC TG GGGTG	TTATCCCTGT
msa277466.2{330_1169NT}		TACAACGTTT	ATTGATGATT	AAC TG GGGTG	TTATCCCTGT
msa277466.2{330_M781}		TACAACGTTT	ATTGATGATT	AAC TG GGGTG	TTATCCCTGT

Table 72: Comparative Sequences relating to SAG0941

Consensus	*****	*****	*****	*****	*****
	1351				1400
msa277466.2{330_090}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_JM9130013}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_18RS21}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_2603}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_A909}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_H36B}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_CJB110}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_COH1}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_M732}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_1169NT}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_M781}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
Consensus	*****	*****	*****	*****	*****
	1401				1450
msa277466.2{330_090}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_JM9130013}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_18RS21}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_2603}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_A909}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_H36B}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_CJB110}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_COH1}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_M732}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_1169NT}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_M781}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
Consensus	*****	*****	*****	*****	*****
	1451				1500
msa277466.2{330_090}	TTCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCC	TACTGTTAAA
msa277466.2{330_JM9130013}	TTCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCC	TACTGTTAAA
msa277466.2{330_18RS21}	TTCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCC	TACTGTTAAA
msa277466.2{330_2603}	TTCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCC	TACTGTTAAA
msa277466.2{330_A909}	TTCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCC	TACTGTTAAA
msa277466.2{330_H36B}	TTCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCC	TACTGTTAAA
msa277466.2{330_CJB110}	TTCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCC	TACTGTTAAA
msa277466.2{330_COH1}	TTCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCC	TACTGTTAAA
msa277466.2{330_M732}	TTCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCC	TACTGTTAAA
msa277466.2{330_1169NT}	TTCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCC	TACTGTTAAA
msa277466.2{330_M781}	TTCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCC	TACTGTTAAA
Consensus	*****	*****	*****	*****	*****

SEQ ID NO. 7212

STRAIN 2603 frame: 1

MNKRKIVATLGPVAFVFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRFNFSHG
 DHAEQGMATVRKAEEIAGQKVGFLDITKGPEIRTELFEDGADFHSYTTGTCLRVATKQ
 GIKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVENDGLI
 GKQGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGX
 GHVKLFAKIEHQGGIDNIDEI IEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGK
 AVITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATID
 KNAQTLLNEYGRLDSSAFPRNNKTDVIA SAVKDATHSMDIKLVVTTITETGNTARAI SKFRP
 PDADILAVTFDEKVRQSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNI VIV
 VAGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7213

STRAIN 090 frame: 1

NKRKIVATLGPVAFVFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRFNFSHGD
 HAEQGMATVRKAEEIAGQKVGFLDITKGPEIRTELFEDGADFHSYTTGTCLRVATKQ
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVENDGLI
 GKQGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGX
 HVKLFAKIEHQGGIDNIDEI IEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRLDSSAFPRNNKTDVIA SAVKDATHSMDIKLVVTTITETGNTARAI SKFRP
 DADILAVTFDEKVRQSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNI VIV
 VAGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7214

STRAIN A909 frame: 1

NKRKIVATLGPVAFVFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRFNFSHGD
 HAEQGMATVRKAEEIAGQKVGFLDITKGPEIRTELFEDGADFHSYTTGTCLRVATKQ
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVENDGLI
 GKQGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGX
 HVKLFAKIEHQGGIDNIDEI IEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRLDSSAFPRNNKTDVIA SAVKDATHSMDIKLVVTTITETGNTARAI SKFRP
 DADILAVTFDEKVRQSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNI VIV
 VAGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7215

STRAIN H36B frame: 1

Table 72: Comparative Sequences relating to SAG0941

NKRVKIVATLGP AVEFRGGKKFGESGYWGESLDVEASA EKIAQLIKEGANVFRNF SHGD
 HAEQGARMATVRKAE E IAGQKVGFLD LTKGPEIRTEL FEDGAD FHSYTTGT KLRVATKQG
 IKSTPEVIALNVAGGLD I FDDVEVGKQ I LVDDGKLG LTVFAKDKD TREFEVVVENDGLIG
 KQKGVNI PYTKI PFPALAE RDNADIRFGL EQGLNFIAISFVRTAKDVNEVRAICBETGNG
 HVKLFAKIENQQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRLDSSAFPRNNKTDV IASAVK DATHSMDIKLVVTITETGNTARAI SKFRP
 DADILAVTFDEKVQ RSLMINWGVIPVLADKPASTDDMF EVAERVALEAGFVESGDNI VIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7216

STRAIN 18RS21 frame: 1

NKRVKIVATLGP AVEFRGGKKFGESGYWGESLDVEASA EKIAQLIKEGANVFRNF SHGD
 HAEQGARMATVRKAE E IAGQKVGFLD LTKGPEIRTEL FEDGAD FHSYTTGT KLRVATKQG
 IKSTPEVIALNVAGGLD I FDDVEVGKQ I LVDDGKLG LTVFAKDKD TREFEVVVENDGLIG
 KQKGVNI PYTKI PFPALAE RDNADIRFGL EQGLNFIAISFVRTAKDVNEVRAICBETGNG
 HVKLFAKIENQQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRLDSSAFPRNNKTDV IASAVK DATHSMDIKLVVTITETGNTARAI SKFRP
 DADILAVTFDEKVQ RSLMINWGVIPVLADKPASTDDMF EVAERVALEAGFVESGDNI VIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7217

STRAIN M732 frame: 1

NKRVKIVATLGP AVEFRGGKKFGESGYWGESLDVEASA EKIAQLIKEGANVFRNF SHGD
 HAEQGARMATVRKAE E IAGQKVGFLD LTKGPEIRTEL FEDGAD FHSYTTGT KLRVATKQG
 IKSTPEVIALNVAGGLD I FDDVEVGKQ I LVDDGKLG LTVFAKDKD TREFEVVVENDGLIG
 KQKGVNI PYTKI PFPALAE RDNADIRFGL EQGLNFIAISFVRTAKDVNEVRAICBETGNG
 HVKLFAKIENQQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRLDSSAFPRNNKTDV IASAVK DATHSMDIKLVVTITETGNTARAI SKFRP
 DADILAVTFDEKVQ RSLMINWGVIPVLADKPASTDDMF EVAERVALEAGFVESGDNI VIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7218

STRAIN COH1 frame: 1

NKRVKIVATLGP AVEFRGGKKFGESGYWGESLDVEASA EKIAQLIKEGANVFRNF SHGD
 HAEQGARMATVRKAE E IAGQKVGFLD LTKGPEIRTEL FEDGAD FHSYTTGT KLRVATKQG
 IKSTPEVIALNVAGGLD I FDDVEVGKQ I LVDDGKLG LTVFAKDKD TREFEVVVENDGLIG
 KQKGVNI PYTKI PFPALAE RDNADIRFGL EQGLNFIAISFVRTAKDVNEVRAICBETGNG
 HVKLFAKIENQQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRLDSSAFPRNNKTDV IASAVK DATHSMDIKLVVTITETGNTARAI SKFRP
 DADILAVTFDEKVQ RSLMINWGVIPVLADKPASTDDMF EVAERVALEAGFVESGDNI VIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7219

STRAIN M781 frame: 1

NKRVKIVATLGP AVEFRGGKKFGESGYWGESLDVEASA EKIAQLIKEGANVFRNF SHGD
 HAEQGARMATVRKAE E IAGQKVGFLD LTKGPEIRTEL FEDGAD FHSYTTGT KLRVATKQG
 IKSTPEVIALNVAGGLD I FDDVEVGKQ I LVDDGKLG LTVFAKDKD TREFEVVVENDGLIG
 KQKGVNI PYTKI PFPALAE RDNADIRFGL EQGLNFIAISFVRTAKDVNEVRAICBETGNG
 HVKLFAKIENQQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRLDSSAFPRNNKTDV IASAVK DATHSMDIKLVVTITETGNTARAI SKFRP
 DADILAVTFDEKVQ RSLMINWGVIPVLADKPASTDDMF EVAERVALEAGFVESGDNI VIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7220

STRAIN CJB110 frame: 1

NKRVKIVATLGP AVEFRGGKKFGESGYWGESLDVEASA EKIAQLIKEGANVFRNF SHGD
 HAEQGARMATVRKAE E IAGQKVGFLD LTKGPEIRTEL FEDGAD FHSYTTGT KLRVATKQG
 IKSTPEVIALNVAGGLD I FDDVEVGKQ I LVDDGKLG LTVFAKDKD TREFEVVVENDGLIG
 KQKGVNI PYTKI PFPALAE RDNADIRFGL EQGLNFIAISFVRTAKDVNEVRAICBETGNG
 HVKLFAKIENQQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRLDSSAFPRNNKTDV IASAVK DATHSMDIKLVVTITETGNTARAI SKFRP
 DADILAVTFDEKVQ RSLMINWGVIPVLADKPASTDDMF EVAERVALEAGFVESGDNI VIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7221

STRAIN 1169NT frame: 1

NKRVKIVATLGP AVEFRGGKKFGESGYWGESLDVEASA EKIAQLIKEGANVFRNF SHGD
 HAEQGARMATVRKAE E IAGQKVGFLD LTKGPEIRTEL FEDGAD FHSYTTGT KLRVATKQG
 IKSTPEVIALNVAGGLD I FDDVEVGKQ I LVDDGKLG LTVFAKDKD TREFEVVVENDGLIG
 KQKGVNI PYTKI PFPALAE RDNADIRFGL EQGLNFIAISFVRTAKDVNEVRAICBETGNG
 HVKLFAKIENQQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRLDSSAFPRNNKTDV IASAVK DATHSMDIKLVVTITETGNTARAI SKFRP
 DADILAVTFDEKVQ RSLMINWGVIPVLADKPASTDDMF EVAERVALEAGFVESGDNI VIV
 AGVPVGTGGTNTMRVRTVK

Table 72: Comparative Sequences relating to SAG0941.

SEQ ID NO. 7222

STRAIN JM9130013 frame: 1

NKRVKIVATLGPVAFRGGKFGESGYWGESLDVEASAEKIAQLIKEGANVFRNFHSHG
 HAEQGMATVRKAEIAGQKVGFLDITKGPETELFEDGSDHFSYTTGKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGITVFAKDKDTREFEVVENDGLIG
 KQKGVNIPYTKIPFPALAEADNADIRFGLGGLNFIAISFVRTAKDVNSVRAICEETGNG
 HVKLFKAIENQOQIDNIDEIIEAADGIMIAARGDMGIEVFPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVDFNAVIDGTDATLMSGESANGKYPVESVTRMATIDK
 NAQTLLENGRLDSSAFPRNKTDVIAASAVKDATHSMDIKLVVTTITETGTARAIKFRP
 DADILAVTFDEKVRSLMINKGVIPLADKPASTDDMFEVAERVALEAGLVESGDNIIVIV
 AGVPVGTGGTNTMRVTVK

PRETTY of: /biotmp/msa277662.2{*} February 24, 2003 01:49 ..

	1		50
msa277662.2{330_18RS21}	~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG
msa277662.2{330_A909}	~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG
msa277662.2{330_CJB110}	~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG
msa277662.2{330_H36B}	~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG
msa277662.2{330_1169NT}	~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG
msa277662.2{330_COH1}	~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG
msa277662.2{330_M732}	~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG
msa277662.2{330_M781}	~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG
msa277662.2{330_JM9130013}	~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG
msa277662.2{330_090}	~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG
msa277662.2{330_2603}	~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG
Consensus	*****	*****	*****

	51		100
msa277662.2{330_18RS21}	NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG
msa277662.2{330_A909}	NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG
msa277662.2{330_CJB110}	NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG
msa277662.2{330_H36B}	NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG
msa277662.2{330_1169NT}	NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG
msa277662.2{330_COH1}	NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG
msa277662.2{330_M732}	NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG
msa277662.2{330_M781}	NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG
msa277662.2{330_JM9130013}	NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG
msa277662.2{330_090}	NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG
msa277662.2{330_2603}	NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG
Consensus	*****	*****	*****

	101		150
msa277662.2{330_18RS21}	DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA
msa277662.2{330_A909}	DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA
msa277662.2{330_CJB110}	DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA
msa277662.2{330_H36B}	DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA
msa277662.2{330_1169NT}	DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA
msa277662.2{330_COH1}	DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA
msa277662.2{330_M732}	DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA
msa277662.2{330_M781}	DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA
msa277662.2{330_JM9130013}	DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA
msa277662.2{330_090}	DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA
msa277662.2{330_2603}	DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA
Consensus	*****	*****	*****

	151		200
msa277662.2{330_18RS21}	VDDGKLGITV	FAKDKDTREF	EVVVENDGLI
msa277662.2{330_A909}	VDDGKLGITV	FAKDKDTREF	EVVVENDGLI
msa277662.2{330_CJB110}	VDDGKLGITV	FAKDKDTREF	EVVVENDGLI
msa277662.2{330_H36B}	VDDGKLGITV	FAKDKDTREF	EVVVENDGLI
msa277662.2{330_1169NT}	VDDGKLGITV	FAKDKDTREF	EVVVENDGLI
msa277662.2{330_COH1}	VDDGKLGITV	FAKDKDTREF	EVVVENDGLI
msa277662.2{330_M732}	VDDGKLGITV	FAKDKDTREF	EVVVENDGLI
msa277662.2{330_M781}	VDDGKLGITV	FAKDKDTREF	EVVVENDGLI
msa277662.2{330_JM9130013}	VDDGKLGITV	FAKDKDTREF	EVVVENDGLI
msa277662.2{330_090}	VDDGKLGITV	FAKDKDTREF	EVVVENDGLI
msa277662.2{330_2603}	VDDGKLGITV	FAKDKDTREF	EVVVENDGLI
Consensus	*****	*****	*****

	201		250
msa277662.2{330_18RS21}	RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE
msa277662.2{330_A909}	RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE
msa277662.2{330_CJB110}	RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE
msa277662.2{330_H36B}	RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE
msa277662.2{330_1169NT}	RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE
msa277662.2{330_COH1}	RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE
msa277662.2{330_M732}	RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE
msa277662.2{330_M781}	RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE
msa277662.2{330_JM9130013}	RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE
msa277662.2{330_090}	RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE
msa277662.2{330_2603}	RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE
Consensus	*****	*****	*****

Table 72: Comparative Sequences relating to SAG0941

	251				300
msa277662.2{330_18RS21}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_A909}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_CJB110}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_H36B}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_1169NT}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_COH1}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_M732}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_M781}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_JM9130013}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_090}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_2603}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
Consensus	*****	*****	*****	*****	*****
	301				350
msa277662.2{330_18RS21}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_A909}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_CJB110}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_H36B}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_1169NT}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_COH1}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_M732}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_M781}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_JM9130013}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_090}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_2603}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
Consensus	*****	*****	*****	*****	*****
	351				400
msa277662.2{330_18RS21}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAA	VKDATHSMDI
msa277662.2{330_A909}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAA	VKDATHSMDI
msa277662.2{330_CJB110}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAA	VKDATHSMDI
msa277662.2{330_H36B}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAA	VKDATHSMDI
msa277662.2{330_1169NT}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAA	VKDATHSMDI
msa277662.2{330_COH1}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAA	VKDATHSMDI
msa277662.2{330_M732}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAA	VKDATHSMDI
msa277662.2{330_M781}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAA	VKDATHSMDI
msa277662.2{330_JM9130013}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAA	VKDATHSMDI
msa277662.2{330_090}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAA	VKDATHSMDI
msa277662.2{330_2603}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAA	VKDATHSMDI
Consensus	*****	*****	*****	*****	*****
	401				450
msa277662.2{330_18RS21}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_A909}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_CJB110}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_H36B}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_1169NT}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_COH1}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_M732}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_M781}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_JM9130013}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_090}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_2603}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
Consensus	*****	*****	*****	*****	*****
	451				500
msa277662.2{330_18RS21}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_A909}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_CJB110}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_H36B}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_1169NT}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_COH1}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_M732}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_M781}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_JM9130013}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_090}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_2603}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
Consensus	*****	*****	*****	*****	*****

Table 73: Comparative Sequences relating to SAG0981

SEQ ID NO. 7301

STRAIN 2603

TTGCTCTATAATAGACAAAAAGGTGGTGATATTTATGTATTTAGCATTAAATCGGTGAT
 ATCATTAAATCAAACAGATACCTGAACGTGAAACCTTCCAAACAGTCTTTTCAGCAACTA
 ATGACCGAAGTATCTGATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCT
 GGTGATGAATTTCAAGCTTTATTGAAACCATCAAAAAGGTATTTCAAATTATTGACCAT
 ATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCGGTACAGGAAACATTATA
 ACATCCATCAATTCAAATGAAAGTATCGGTGCTGATGGTCTGCCTACTGGCATGCTCGC
 TCAGCTATTAAATCATATACATGATAAAATGATTATGGAACAGTTCAAGTAGCTATTGTC
 CTTGATGATGAAGACCAAAACCTTGAATTAACACTAAATAGTCTCATTTTCAGCTGGTGAT
 TTTATCAAGTCAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAA
 GATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGGAAAATATTGAACCT
 AGTGCCTGACTAAACGCCCTTAAAGCAAGCGGTCTGAAGATTACTTAAAGAACGAGAACA
 CAGGCAGCCGATCTATTAGTTAAAGTTGCACCTCAAACTAAAGGGGAAGCTATGATTTC

SEQ ID NO. 7302

STRAIN 090

TCTGCTATAATAGACAAAAAGGTGGTGATATTTATGTATTT
 AGCATTAAATCGGTGATATCATTAAATCAAACAGATACCTGAACGTGAAA
 CTTTCCAAACAGTCTTTTCAGCAACTAATGACCGAAGTATCTGATGTATAT
 GGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGATGAATTTCA
 AGCTTTATTGAAACCATCAAAAAGGTATTTCAAATTATTGACCATATTTC
 AACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCGGTACAGGAAAC
 ATTATAACATCCATCAATTTAAATGAAAGTATCGGTGCTGATGGTCTGCTG
 CTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAAAATGATT
 ATGGAACAGTTTCAAGTAGCTATTGCTTGGATGATGAAGACCAAAACCTT
 GAATTAACACTAAATAGTCTCATTTTCAGCTGGTGATTTTATCAAGTCAAA
 ATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAAGATA
 ATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGGAAAATATT
 GAACCTAGTGCCTGACTAAACGCCCTTAAAGCAAGCGGTCTGAAGATTTA
 CTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAGTTGCACCT
 AAATAAGGGGAAGCTATGATTTC

SEQ ID NO. 7303

STRAIN A909

TCTGCTATAATAGACAAAAAGGTGGTGATATTTATGTAT
 TTAGCATTAAATCGGTGATATCATTAAATCAAACAGATACCTGAACGTGA
 AACTTTCCAAACAGTCTTTTCAGCAACTAATGACCGAAGTATCTGATGTAT
 ATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGATGAATTT
 CAAGCTTTATTGAAACCATCAAAAAGGTATTTCAAATTATTGACCATAT
 TCAACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCGGTACAGGAA
 ACATTATAACATCCATCAATTTCAAATGAAAGTATCGGTGCTGATGGTCTCT
 GCCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAAAATGA
 TTATGGAACAGTTCAAGTAGCTATTGCTTGGATGATGAAGACCAAAACCT
 TTGAATTAAACACTAAATAGTCTCATTTTCAGCTGGTGATTTTATCAAGTCA
 AAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAAGA
 TAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGGAAAATA
 TTGAACCTAGTGCCTGACTAAACGCCCTTAAAGCAAGCGGTCTGAAGATT
 TACTTAAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAGTTGCAC
 TCAAACTAAAGGGGAAGCTATGATTTC

SEQ ID NO. 7304

STRAIN H36B

TCTGCTATAATAGACAAAAAGGTGGTGATATTT
 ATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAACAGATACCTTGA
 ACGTGAACCTTTCCAAACAGTCTTTTCAGCAACTAATGACCGAAGTATCTG
 ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
 GAATTTCAAGCTTTATTGAAACCATCAAAAAGGTATTTCAAATTATTGA
 CCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCGGTA
 CAGGAACATTATAACATCCATCAATTTCAAATGAAAGTATCGGTGCTGAT
 GGTCTGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAA
 AAATGATTATGGAACAGTTCAAGTAGCTATTGCTTGGATGATGAAGACC
 AAAACCTTGAATTAAACACTAAATAGTCTCATTTTCAGCTGGTGATTTTATC
 AAGTCAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT
 TCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGG
 AAAATATTGAACCTAGTGCCTGACTAAACGCCCTTAAAGCAAGCGGTCTG
 AAGATTTACTTAAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 TTGCACTCAAACTAAAGGGGAAGCTATGATTTC

SEQ ID NO. 7305

STRAIN 18RS21

TCTGCTATAATAGACAAAAAGGTGGTGATATTT
 ATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAACAGATACCTTGA
 ACGTGAACCTTTCCAAACAGTCTTTTCAGCAACTAATGACCGAAGTATCTG
 ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
 GAATTTCAAGCTTTATTGAAACCATCAAAAAGGTATTTCAAATTATTGA
 CCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCGGTA
 CAGGAACATTATAACATCCATCAATTTCAAATGAAAGTATCGGTGCTGAT
 GGTCTGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAA
 AAATGATTATGGAACAGTTCAAGTAGCTATTGCTTGGATGATGAAGACC
 AAAACCTTGAATTAAACACTAAATAGTCTCATTTTCAGCTGGTGATTTTATC
 AAGTCAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT
 TCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGG
 AAAATATTGAACCTAGTGCCTGACTAAACGCCCTTAAAGCAAGCGGTCTG
 AAGATTTACTTAAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 TTGCACTCAAACTAAAGGGGAAGCTATGATTTC

Table 73: Comparative Sequences relating to SAG0981

TCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGG
 AAAATATTGAACCTAGTGCCTGACTAAACGCCCTTAAAGCAAGCGGTCTG
 AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 TTGCACTCAAACCTAAAGGGGAAGCTATGATTTC

SEQ ID NO. 7306

STRAIN M732

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 TATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACTTG
 AACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCT
 GATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGA
 TGAATTTCAAGCTTTATTTGAAACaATCAAAAAAGGTATTTCAAATTTATTG
 ACCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGCCCTCGGT
 ACAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGA
 TGGTCTGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATA
 AAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGAC
 CAAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTAT
 CAAGTCAAAATGGACTACAAACCAATTTCAAATGCTTGAGCACTTAATAC
 TTCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTG
 GAAAATATTGAACCTAGTGCCTGACTAAACGCCCTTAAAGCAAGCGGTCT
 GAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAA
 GTTGCACTCAAACCTAAAGGGGAAGCTATGATTTC

SEQ ID NO. 7307

STRAIN COH1

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 TATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACTTG
 AACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCT
 GATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGA
 TGAATTTCAAGCTTTATTTGAAACaATCAAAAAAGGTATTTCAAATTTATTG
 ACCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGCCCTCGGT
 ACAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGA
 TGGTCTGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATA
 AAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGAC
 CAAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTAT
 CAAGTCAAAATGGACTACAAACCAATTTCAAATGCTTGAGCACTTAATAC
 TTCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTG
 GAAAATATTGAACCTAGTGCCTGACTAAACGCCCTTAAAGCAAGCGGTCT
 GAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAA
 GTTGCACTCAAACCTAAAGGGGAAGCTATGATTTC

SEQ ID NO. 7308

STRAIN M781

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 ATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACTTGA
 ACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG
 ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
 GAATTTCAAGCTTTATTTGAAACaATCAAAAAAGGTATTTCAAATTTATTGA
 CCAATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGCCCTCGGTGA
 CAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT
 GGTCTGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAA
 AATGATTATGGAACAGTTCAAGTAGCTATTTGCCITGATGATGAAGACC
 AAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTATC
 AAGTCAAAATGGACTACAAACCAATTTCAAATGCTTGAGCACTTAATACT
 TCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGG
 AAAATATTGAACCTAGTGCCTGACTAAACGCCCTTAAAGCAAGCGGTCTG
 AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 TTGCACTCAAACCTAAAGGGGAAGCTATGATTTC

SEQ ID NO. 7309

STRAIN CJB110

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 TTTATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACT
 TGAACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTAT
 CTGATGTATATGGTGAAGAGCTGATTTCTCTATTCACTATTACAGCTGGT
 GATGAATTTCAAGCTTTATTTGAAACCATCAAAAAAGGTATTTCAAATTTAT
 TGACCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGCCCTCG
 GTACAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCT
 GATGGTCTGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATA
 TAAAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCITGATGATGAAG
 ACCAAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTT
 ATCAAGTCAAAATGGACTACTAACCAATTTCAAATGCTTGAGCACTTAAT
 ACTTCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACT
 TGGAAAATATTGAACCTAGTGCCTGACTAAACGCCCTTAAAGCAAGCGGT
 CTGAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAA
 AAGTTGCACTCAAACCTAAAGGGGAAGCTATGATTTC

SEQ ID NO. 7310

STRAIN JM9130013

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 ATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACTTGA
 ACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG

Table 73: Comparative Sequences relating to SAG0981

ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT GAATTTCAAGCTTTATGAAACCATCAAAAAAGGTATTTCAAATTATTGA CCATATTCAACTAGCTCTAAACCTGTTAATGTAAGGTTCCGGCTCGGTA CAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT GGTCTGCTACTGCGCATGCTCGCTCAGCTATTATCATATACATGATAA AAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACC AAAACCTTGAATTAAACACTAAATAGTCTCATTTCAGCTGGTGATTTTATC AAGTCAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT TCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCACTGG AAAATATTGAACCTAGTGCCTGACTAAACGCCTTAAGCAAGCGGTCTG AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG TTGCACTCAAATAAAGGGGAAGCTATGATTTTC					
PRETTY of: /biotmp/msa31912.2{*} February 18, 2003 08:19 ..					
msa31912.2{338_18RS21}	1	50			
msa31912.2{338_2603}	---TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT
msa31912.2{338_A909}	ttgTCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT
msa31912.2{338_H36B}	---TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT
msa31912.2{338_JM9130013}	---TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT
msa31912.2{338_COH1}	---TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT
msa31912.2{338_M732}	---TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT
msa31912.2{338_M781}	---TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT
msa31912.2{338_090}	---TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT
msa31912.2{338_CJB110}	---TCTGCTA	TAATAGACAA	AAAGGTGGTG	gTATTTATGT	ATTAGCATT
Consensus	*****	*****	*****	*****	*****
msa31912.2{338_18RS21}	51	100			
msa31912.2{338_2603}	AATCGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
msa31912.2{338_A909}	AATCGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
msa31912.2{338_H36B}	AATCGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
msa31912.2{338_JM9130013}	AATCGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
msa31912.2{338_COH1}	AATCGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
msa31912.2{338_M732}	AATCGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
msa31912.2{338_M781}	AATCGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
msa31912.2{338_090}	AATCGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
msa31912.2{338_CJB110}	AATCGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
Consensus	*****	*****	*****	*****	*****
msa31912.2{338_18RS21}	101	150			
msa31912.2{338_2603}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
msa31912.2{338_A909}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
msa31912.2{338_H36B}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
msa31912.2{338_JM9130013}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
msa31912.2{338_COH1}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
msa31912.2{338_M732}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
msa31912.2{338_M781}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
msa31912.2{338_090}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
msa31912.2{338_CJB110}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
Consensus	*****	*****	*****	*****	*****
msa31912.2{338_18RS21}	151	200			
msa31912.2{338_2603}	GAGCTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
msa31912.2{338_A909}	GAGCTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
msa31912.2{338_H36B}	GAGCTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
msa31912.2{338_JM9130013}	GAGCTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
msa31912.2{338_COH1}	GAGCTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
msa31912.2{338_M732}	GAGCTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
msa31912.2{338_M781}	GAGCTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
msa31912.2{338_090}	GAGCTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
msa31912.2{338_CJB110}	GAGCTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
Consensus	*****	*****	*****	*****	*****
msa31912.2{338_18RS21}	201	250			
msa31912.2{338_2603}	ATTGAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
msa31912.2{338_A909}	ATTGAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
msa31912.2{338_H36B}	ATTGAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
msa31912.2{338_JM9130013}	ATTGAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
msa31912.2{338_COH1}	ATTGAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
msa31912.2{338_M732}	ATTGAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
msa31912.2{338_M781}	ATTGAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
msa31912.2{338_090}	ATTGAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
msa31912.2{338_CJB110}	ATTGAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
Consensus	*****	*****	*****	*****	*****
msa31912.2{338_18RS21}	251	300			
msa31912.2{338_2603}	CTCTAAACC	TGTTAATGTA	AGGTTCCGCC	TCGGTACAGG	AAACATTATA
	CTCTAAACC	TGTTAATGTA	AGGTTCCGCC	TCGGTACAGG	AAACATTATA

Table 73: Comparative Sequences relating to SAG0981

msa31912.2{338_A909}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA		
msa31912.2{338_H36B}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA		
msa31912.2{338_JM9130013}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA		
msa31912.2{338_COH1}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA		
msa31912.2{338_M732}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA		
msa31912.2{338_M781}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA		
msa31912.2{338_090}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA		
msa31912.2{338_CJB110}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA		
Consensus	*****	*****	*****	*****	*****		
msa31912.2{338_18RS21}	301	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	350	CTGCCTACTG
msa31912.2{338_2603}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
msa31912.2{338_A909}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
msa31912.2{338_H36B}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
msa31912.2{338_JM9130013}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
msa31912.2{338_COH1}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
msa31912.2{338_M732}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
msa31912.2{338_M781}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
msa31912.2{338_090}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
msa31912.2{338_CJB110}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
Consensus	*****	***_*****	*****	*****	*****		
msa31912.2{338_18RS21}	351	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	400	GATTATGGAA
msa31912.2{338_2603}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
msa31912.2{338_A909}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
msa31912.2{338_H36B}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
msa31912.2{338_JM9130013}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
msa31912.2{338_COH1}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
msa31912.2{338_M732}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
msa31912.2{338_M781}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
msa31912.2{338_090}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
msa31912.2{338_CJB110}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
Consensus	*****	*****	*****	*****	*****		
msa31912.2{338_18RS21}	401	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	450	CCTTGAATTA
msa31912.2{338_2603}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
msa31912.2{338_A909}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
msa31912.2{338_H36B}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
msa31912.2{338_JM9130013}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
msa31912.2{338_COH1}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
msa31912.2{338_M732}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
msa31912.2{338_M781}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
msa31912.2{338_090}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
msa31912.2{338_CJB110}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
Consensus	*****	*****	*****	*****	*****		
msa31912.2{338_18RS21}	451	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	500	CAAAATGGAC
msa31912.2{338_2603}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
msa31912.2{338_A909}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
msa31912.2{338_H36B}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
msa31912.2{338_JM9130013}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
msa31912.2{338_COH1}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
msa31912.2{338_M732}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
msa31912.2{338_M781}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
msa31912.2{338_090}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
msa31912.2{338_CJB110}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
Consensus	*****	*****	*****	*****	*****		
msa31912.2{338_18RS21}	501	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	550	GATAAATTATC
msa31912.2{338_2603}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
msa31912.2{338_A909}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
msa31912.2{338_H36B}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
msa31912.2{338_JM9130013}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
msa31912.2{338_COH1}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
msa31912.2{338_M732}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
msa31912.2{338_M781}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
msa31912.2{338_090}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
msa31912.2{338_CJB110}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
Consensus	***-*****	*****	*****	*****	*****		
msa31912.2{338_18RS21}	551	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AAGTTAGCCC	600	TATTGAACCT
msa31912.2{338_2603}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AAGTTAGCCC	TATTGAACCT		
msa31912.2{338_A909}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AAGTTAGCCC	TATTGAACCT		
msa31912.2{338_H36B}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AAGTTAGCCC	TATTGAACCT		
msa31912.2{338_JM9130013}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AAGTTAGCCC	TATTGAACCT		
msa31912.2{338_COH1}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AAGTTAGCCC	TATTGAACCT		
msa31912.2{338_M732}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AAGTTAGCCC	TATTGAACCT		

Table 73: Comparative Sequences relating to SAG0981

msa31912.2{338_M781}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT		
msa31912.2{338_090}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT		
msa31912.2{338_CJB110}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT		
Consensus	*****	*****	*****	*****	*****		
msa31912.2{338_18RS21}	601	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG	650
msa31912.2{338_2603}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG		
msa31912.2{338_A909}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG		
msa31912.2{338_H36B}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG		
msa31912.2{338_JM9130013}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG		
msa31912.2{338_COH1}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG		
msa31912.2{338_M732}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG		
msa31912.2{338_M781}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG		
msa31912.2{338_090}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG		
msa31912.2{338_CJB110}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG		
Consensus	*****	*****	*****	*****	*****		
msa31912.2{338_18RS21}	651	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA	700
msa31912.2{338_2603}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA		
msa31912.2{338_A909}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA		
msa31912.2{338_H36B}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA		
msa31912.2{338_JM9130013}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA		
msa31912.2{338_COH1}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA		
msa31912.2{338_M732}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA		
msa31912.2{338_M781}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA		
msa31912.2{338_090}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA		
msa31912.2{338_CJB110}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA		
Consensus	*****	*****	*****	*****	*****		
msa31912.2{338_18RS21}	701	AAGGGGGAAG	CTATGATTTC				720
msa31912.2{338_2603}	AAGGGGGAAG	CTATGATTTC					
msa31912.2{338_A909}	AAGGGGGAAG	CTATGATTTC					
msa31912.2{338_H36B}	AAGGGGGAAG	CTATGATTTC					
msa31912.2{338_JM9130013}	AAGGGGGAAG	CTATGATTTC					
msa31912.2{338_COH1}	AAGGGGGAAG	CTATGATTTC					
msa31912.2{338_M732}	AAGGGGGAAG	CTATGATTTC					
msa31912.2{338_M781}	AAGGGGGAAG	CTATGATTTC					
msa31912.2{338_090}	AAGGGGGAAG	CTATGATTTC					
msa31912.2{338_CJB110}	AAGGGGGAAG	CTATGATTTC					
Consensus	*****	*****					
SEQ ID NO. 7311							
STRAIN 2603 frame: 1							
LSAIDKKVVFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFITITA							
GDEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHAR							
SAINHIHDKNDYGTGVQVAICLDDQNLLETLNLSISAGDFIKSKWTTNHFQMLEHLILQ							
DNYQEQFHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCQTQTKGGSYDF							
SEQ ID NO. 7312							
STRAIN 090 frame: 1							
SAIDKKVVFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFITITAG							
DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINL NESIGADGPAYWHARS							
AINHIHDKNDYGTGVQVAICLDDQNLLETLNLSISAGDFIKSKWTTNHFQMLEHLILQD							
NYQEQFHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCQTQTKGGSYDF							
SEQ ID NO. 7313							
STRAIN A909 frame: 1							
SAIDKKVVFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFITITAG							
DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS							
AINHIHDKNDYGTGVQVAICLDDQNLLETLNLSISAGDFIKSKWTTNHFQMLEHLILQD							
NYQEQFHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCQTQTKGGSYDF							
SEQ ID NO. 7314							
STRAIN H36B frame: 1							
SAIDKKVVFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFITITAG							
DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS							
AINHIHDKNDYGTGVQVAICLDDQNLLETLNLSISAGDFIKSKWTTNHFQMLEHLILQD							
NYQEQFHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCQTQTKGGSYDF							
SEQ ID NO. 7315							
STRAIN 18RS21 frame: 1							
SAIDKKVVFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFITITAG							
DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS							
AINHIHDKNDYGTGVQVAICLDDQNLLETLNLSISAGDFIKSKWTTNHFQMLEHLILQD							
NYQEQFHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCQTQTKGGSYDF							
SEQ ID NO. 7316							
STRAIN M732 frame: 1							
SAIDKKVVFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFITITAG							

Table 73: Comparative Sequences relating to SAG0981

DEFQALLKQSKKVFQIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTGVQVAICLDDDEDQNLLELTNLSISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENI EPSALT KRKLKASGLKIYLRTRTQAADLLVKSCQTQTKGGSYDF

SEQ ID NO. 7317

STRAIN COH1 frame: 1

SAIIDKKVVFMYLALIGDI INSKQILERETFQQS FQQLMTELS DVYGEELIS PFTITAG
 DEFQALLKQSKKVFQIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTGVQVAICLDDDEDQNLLELTNLSISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENI EPSALT KRKLKASGLKIYLRTRTQAADLLVKSCQTQTKGGSYDF

SEQ ID NO. 7318

STRAIN M781 frame: 1

SAIIDKKVVFMYLALIGDI INSKQILERETFQQS FQQLMTELS DVYGEELIS PFTITAG
 DEFQALLKQSKKVFQIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTGVQVAICLDDDEDQNLLELTNLSISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENI EPSALT KRKLKASGLKIYLRTRTQAADLLVKSCQTQTKGGSYDF

SEQ ID NO. 7319

STRAIN CJB110 frame: 1

SAIIDKKVVFMYLALIGDI INSKQILERETFQQS FQQLMTELS DVYGEELIS PFTITAG
 DEFQALLKQSKKVFQIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTGVQVAICLDDDEDQNLLELTNLSISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENI EPSALT KRKLKASGLKIYLRTRTQAADLLVKSCQTQTKGGSYDF

SEQ ID NO. 7320

STRAIN JM9130013 frame: 1

SAIIDKKVVFMYLALIGDI INSKQILERETFQQS FQQLMTELS DVYGEELIS PFTITAG
 DEFQALLKQSKKVFQIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTGVQVAICLDDDEDQNLLELTNLSISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENI EPSALT KRKLKASGLKIYLRTRTQAADLLVKSCQTQTKGGSYDF

PRETTY of: /biotmp/msa32053.2{*} February 18, 2003 08:25 ..

	1		50
msa32053.2{338_18RS21}	~SAIIDKKVV	iFMYLALIGD	I INSKQILER
msa32053.2{338_2603}	~SAIIDKKVV	iFMYLALIGD	I INSKQILER
msa32053.2{338_909}	~SAIIDKKVV	iFMYLALIGD	I INSKQILER
msa32053.2{338_CJB110}	~SAIIDKKVV	vFMYLALIGD	I INSKQILER
msa32053.2{338_COH1}	~SAIIDKKVV	iFMYLALIGD	I INSKQILER
msa32053.2{338_H36B}	~SAIIDKKVV	iFMYLALIGD	I INSKQILER
msa32053.2{338_JM9130013}	~SAIIDKKVV	iFMYLALIGD	I INSKQILER
msa32053.2{338_M732}	~SAIIDKKVV	iFMYLALIGD	I INSKQILER
msa32053.2{338_M781}	~SAIIDKKVV	iFMYLALIGD	I INSKQILER
msa32053.2{338_090}	~SAIIDKKVV	iFMYLALIGD	I INSKQILER
Consensus	*****	-*****	*****

	51		100
msa32053.2{338_18RS21}	ELISpFTITA	GDEFQALLKp	SKKVFQIIDH
msa32053.2{338_2603}	ELISpFTITA	GDEFQALLKp	SKKVFQIIDH
msa32053.2{338_909}	ELISpFTITA	GDEFQALLKp	SKKVFQIIDH
msa32053.2{338_CJB110}	ELISpFTITA	GDEFQALLKp	SKKVFQIIDH
msa32053.2{338_COH1}	ELISpFTITA	GDEFQALLKq	SKKVFQIIDH
msa32053.2{338_H36B}	ELISpFTITA	GDEFQALLKp	SKKVFQIIDH
msa32053.2{338_JM9130013}	ELISpFTITA	GDEFQALLKp	SKKVFQIIDH
msa32053.2{338_M732}	ELISpFTITA	GDEFQALLKq	SKKVFQIIDH
msa32053.2{338_M781}	ELISpFTITA	GDEFQALLKq	SKKVFQIIDH
msa32053.2{338_090}	ELISpFTITA	GDEFQALLKp	SKKVFQIIDH
Consensus	****-****	*****	*****

	101		150
msa32053.2{338_18RS21}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_2603}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_909}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_CJB110}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_COH1}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_H36B}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_JM9130013}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_M732}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_M781}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_090}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
Consensus	****-****	*****	*****

	151		200
msa32053.2{338_18RS21}	TLNSLSISAGD	FIKSKWTTNH	FQMLEHLILQ
msa32053.2{338_2603}	TLNSLSISAGD	FIKSKWTTNH	FQMLEHLILQ
msa32053.2{338_909}	TLNSLSISAGD	FIKSKWTTNH	FQMLEHLILQ
msa32053.2{338_CJB110}	TLNSLSISAGD	FIKSKWTTNH	FQMLEHLILQ
msa32053.2{338_COH1}	TLNSLSISAGD	FIKSKWTTNH	FQMLEHLILQ
msa32053.2{338_H36B}	TLNSLSISAGD	FIKSKWTTNH	FQMLEHLILQ
msa32053.2{338_JM9130013}	TLNSLSISAGD	FIKSKWTTNH	FQMLEHLILQ
msa32053.2{338_M732}	TLNSLSISAGD	FIKSKWTTNH	FQMLEHLILQ
msa32053.2{338_M781}	TLNSLSISAGD	FIKSKWTTNH	FQMLEHLILQ
Consensus	TLNSLSISAGD	FIKSKWTTNH	FQMLEHLILQ

Table 73: Comparative Sequences relating to SAG0981

msa32053.2{338_090}	TLNSLISAGD	FIKSKWTTNH	FQMLEHLILQ	DNYQEQFQHQ	KLAQLENIEP
Consensus	*****	*****	*****	*****	*****
	201			240	
msa32053.2{338_18RS21}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_2603}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_A909}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_CJB110}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_COH1}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_H36B}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_JM9130013}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_M732}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_M781}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_090}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
Consensus	*****	*****	*****	*****	

Table 74: Comparative Sequences relating to SAG1572

SEQ ID NO. 7401

STRAIN 2603

ATGGAAATGCAAGTTCAAAAAGTTTAAATCAAATATACATTACGGAACACTCTAT
CTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGCCATTAGGATTTTA
AGAGAAGTTGATTTTATTGTGTCAGAGGATACACGAAATACGGGACTTTTACTCAAGCAC
TTTGATATTACTACTAAACAAATTAGTTTTCACGAAACAAATGCTTACGATAAAATCTCT
GGGTTAATTGATTTGTTAAAGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATG
CCCTCTATTTCGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCCA
GTTGTATCTATACCAAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTCAGGTTTAGCT
CCACAACCTCATATTTTATTGGCTTCTTACCTCGTAAGAAAGGTCAACAAATAACTTTC
TTTGAAACAAAGCAAGATTACCTGAAACACAAATCTTTATGAGTCACCGTTTCGAGTC
TCTGATACGCTAAACACATGAAAGAGATTTCGGGAGATCGCCAAGTTGTTTTAGTACGC
GAATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCAATTAGTCAACTTTTAGAGCAT
ATTGAAAGAGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGGTAAAGAGATACC
GAGCGAGTGAAGACAGTAGCCAACAAGATCCACTAGTATTAGTAAAGAATATATCGCT
AATGGTGATAAACTAATCAAGCGATAAAAAAGTAGCAAAAGAATTTAATCTCAATAGA
CAAGAACTCTATGCTAGTTCCATGATTTA

SEQ ID NO. 7402

STRAIN 090

GAAATGCAAGTTCAAAAAGTTTAAATCAAATACACATTACGGGACACT
CTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTG
CCATTAGGATTTTAAGAGAAGTTGATTTTATTGTGTCAGAGGATACACGA
AATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTAG
TTTTACGAAACAAATGCTTACGATAAAATCTCTGGGTTAATTGATTTGT
TAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCT
ATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGGGAT
CCCGTCTGATCTATACCAAGGAGCTAGCGCTGGTATTACTGCTCTCATCG
CTTCAGGTTTAGCTCCACAACCTCATATTTTATGGCTTCTTACCGCGT
AAGAAAGGTCAACAAATACTTTTGTGAAACAAAGAAAGATTACCCCTGa
AACAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTAAAC
ACATGAAGAGATTACGGAGATCGCCAAGTTGTTTAGTACGCGAATTG
ACGAACTCTATGAAGAGTATCAAAGAGGAACCAATTAGTCAACTTTTAGG
GCATATTGAAAAAGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATG
GTAAGAGAGATACCGAGCGAGTGAAGACAGTAGCCAACAAGATCCACTA
GTATTAGTAA

SEQ ID NO. 7403

STRAIN A909

AGTTCAAAAAAGTTTAAATCAAATATACATTACGGAACACTCTATCTAG
TCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGCCATTAGG
ATTTAAGAGAAGTTGATTTTATTGTGTCAGAGGATACACGAAATACGGG
ACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTAGTTTTCAGC
AACAATGCTTACGATAAAATCTCTGGGTTAATTGATTTGTTAAAGAA
GGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCTATTCTGA
CCCGAGCATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCAGTTG
TATCTATACCAAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTCAGT
TTAGCTCCACAACCTCATATTTTATGGCTTCTTACCACGTAAGAAAGG
TCAACAAATAACTTTCTTTGAACAAAGCAAGATTACCTGAAACACAAA
TCTTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTAAACACATGAAA
GAGATTACCGAGATCGCCAAGTTGTTTAGTACGCGAATTGACGAAACT
CTATGAAGAGTATCAAAGAGGAACCAATTAGTCAACTTTTAGAGCATATTG
AAAAGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGGTAAAGAGA
GATACCGAGCGAGTGAAGACAGTAGCCAACAAGATCCACTAGTATTAGT
AA

SEQ ID NO. 7404

STRAIN H36B

GAAATGCAAGTTCAAAAAGTTTAAATCAAATACACATT
ACGGGACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATG
ACTTTTCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTGTGTCAGA
GGATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTA
AACAAATTAGTTTTCACGAACACAATGCTTATGATAAAATCTCTGGGTTA
ATTGATTGTGTTAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGG
AATGCCCTCTATTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTG
AAGGGGATATCCCGTCTATCTATACCAAGGAGCTAGCGCTGGTATTACT
GCTCTCATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTATGGCTT
CTTACCGGTAAGCAAGGTCAACAAATAACTTTTGTGAAACAAAGAAAG
ATTACCTGAAACACAAATCTTTATGAGTCACCGTTTCGAGTCTCTGAT
ACGCTAAACACATGAAAGAGATTATGGAGATCGCCAAGTTGTTTAGT
ACCGAATTGACGAACTCTATGAAGAGTATCAAAGAGGAACCAATTAGT
AACTTTTAGGGCATATTGAAAAAGTCCCTCTCAAAGGTGAATGCTTAATT
ATTGTTGATGGTAAAGAGATACGAGCGAGTGAAGACAGTAGCCAACA
AGATCCACTAGTATTAGTAA

SEQ ID NO. 7405

STRAIN 18RS21

GAAATGCAAGTTCAAAAAGTTTAAATCAAATATACATT
ACGGAACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATG
ACTTTTCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTGTGTCAGA
GGATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTA
AACAAATTAGTTTTCACGAACACAATGCTTACGATAAAATCTCTGGGTTA
ATTGATTGTGTTAAAGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGG

Table 74: Comparative Sequences relating to SAG1572

AATGCCCTCTATTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTG
AAGGGGATATCCAGTTGTATCTATACCAGGAGCTAGCGCTGGTATTACT
GCTCTCATCGCTTCAGTTTGTCTCCACACCTCATATTTTTTATGGCTT
CTTACCACGTAAGAAAGGTCAACAAATAACTTTCTTGAAACAAAGCAAG
ATTACCCCTGAAACACAAATCTTTATGAGTCACCGTTTCGAGTCTCTGAT
ACGCTAAACACATGAAAGAGATTACGGAGATCGCCAAGTTGTTTAGT
ACGCGAATTGACGAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTC
AACTTTTAGAGCATATTGAAAGGTCCCTCTCAAAGGTGAATGCTTAATT
ATTGTTGATGGTAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACA
AGATCCACTAGTATTAGTAA

SEQ ID NO. 7406

STRAIN M732

GAAATGCAAGTTCAAAAAAGTTTAAATCAAAT
ATACATTACGGAACACTCTATCTAGTCCCACTCCAATTGGTAATCTAGA
TGATATGACTTTTCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTT
GTGAGAGGATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATT
ACTACTAAACAAATTAGTTTTCACGAACCAATGCTTACGATAAAATCTC
TGGGTTAATTGATTTGTAAAGAAGGGAAATCTTTAGCCCAAGTATCTG
ATGACGGAATGCCCTCTATTCTGACCCAGGACATGACCTTGTCAAGGCT
GCTATTGAAGGGGATATCCAGTTGTATCTATACCAGGAGCTAGCGCTGG
TATTACTGCTCTCATCGCTTCAGTTTACTCCCAACCTCATATTTTTT
ATGGCTTCTTACCACGTAAGAAAGGTCAACAAATAACTTTCTTGAAACA
AAGCAAGATTACCTGAAACACAAATCTTTTATGAGTCACCGTTTCGAGT
CTCTGATACGCTAAACACATGAAAGAGATTACGGAGATCGCCAAGTTG
TTTTAGTACGCGAATTGACGAACTCTATGAAGAGTATCAAAGAGGAACC
ATTAGTCAACTTTTAGAGCATATTGAAAGGTCCCTCTCAAAGGTGAATG
CTTAATTATGTTGATGGTAAGAGAGATACCGAGCGAGTGAAAGACAGTA
GCCAACAGATCCACTAGTATTAGTAA

SEQ ID NO. 7407

STRAIN COH1

GAAATGCAAGTTCAAAAAAGTTTAAATCAAATATACATTAC
GGAACACTCTATCTAGTCCCACTCCAATTGGTAATCTAGATGATATGAC
TTTTCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGAGAGG
ATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAA
CAAAATAGTTTTCACGAACCAATGCTTACGATAAAATCTCTGGGTTAAT
TGATTTGTGTAAGAAGGGGAAATCTTTAGCCCAAGTATCTGATGACGAGAA
TGCCCTCTATTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAA
GGGGATATCCAGTTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGC
TCTCATCGCTTCAGGTTTAGCTCCCAACCTCATATTTTTTATGGCTTCT
TACCAGTTAAGAAAGGTCAACAAATAACTTTCTTGAAACAAAGCAAGAT
TACCCTGAAACACAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGATAC
GCTAAACACATGAAAGAGATTACGGAGATCGCCAAGTTGTTTATGATC
GCGAATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAA
CTTTTAGAGCATATTGAAAGGTCCCTCTCAAAGGTGAATGCTTAATTAT
TGTTGATGGTAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACAAG
ATCCACTAGTATTAGTAA

SEQ ID NO. 7408

STRAIN M781

AAATGCAAGTTCAAAAAAGTTTAAATCAAATATACATTACGGAACACTC
TATCTAGTCCCACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGC
CATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGAGAGGATACACGAA
ATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATAGT
TTTACGAACACAAATGCTTACGATAAAATCTCTGGGTTAATTGATTTGTT
AAAAAGAGGGAAATCTTTAGCCCAAGTATCTGATGACGGAATGCCCTCTA
TTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATC
CCAGTTGTATCTATACAGGAGCTAGCGCTGGTATTACTGCTCTCATCGC
TTCAGGTTTAGCTCCCAACCTCATATTTTTTATGGCTTCTTACCAGTA
AGAAAGGTCAACAAATAACTTTCTTGAAACAAAGCAAGATTACCCTGAA
ACACAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTAAACAC
CATGAAAGAGATTACGGAGATCGCCAAGTTGTTTATGATACGGAATTGA
CGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAGAG
CATATTGAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATGTTGATGG
TAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTAG
TATTAGTAA

A

SEQ ID NO. 7409

STRAIN CJB110

GAAATGCAAGTTCAAAAAAGTTTAAATCAAATACATTACGGGACAC
TCTATCTAGTCCCACTCCAATTGGTAATCTAGATGATATGACTTTTCGT
GCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGAGAGGATACACG
AAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTA
GTTTTACGAACACAAATGCTTACGATAAAATCTCTGGGTTAATTGATTTG
TTAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGACGGAATGCCCTC
TATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGGGA
TCCCGGTGCTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATC
GCTTCAGGTTTAGCTCCCAACCTCATATTTTTTATGGCTTCTTACCAGG
TAAGAAAGGTCAACAAATAACTTTCTTGAAACAAAGAAAGATTACCCTG
AAACACAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTAAAC
CATGAAAGAGATTACGGAGATCGCCAAGTTGTTTATGATACGCGAATT

Table 74: Comparative Sequences relating to SAG1572

GACGAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAG
GGCATATTGAAAAAGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGAT
GGTAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACAGATCCACT
AGTATTAGTAA

SEQ ID NO. 7410

STRAIN 1169NT

TGCAAGTTCAAAAAAGTTTAAATCAAATACACATTATGGGACACTCTAT
CTAGTCCCACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGCCAT
TAGGATTTTAAGAGAGTTGaTTTATTGTGTCAGAGGATACAGAAATA
CGGCACITTTACTCAAGCCTTTGATaTTACTACTAAACAAATTAGtTTT
cACGAACACAATGCTTACGATAAAATCTCTGGGTTAATTGATTtGTTAAA
AGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCTATT
CTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCCA
GTTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTC
AGGTTTAGCTCCACAACCTCATATTTTATGGCTTCTTACCACGTAAGA
AAGGTCAACAAATAACTTTTGTGAAACAAGCAAGATTATCTGAAACA
CAAATCTTTTATGAGTACCGGtTTGAGTCTCTGATACGCTAAACACAT
GAAAGAGATTTACGGAGATCGCCAAGTTGTTTATGACGCAATTGACgA
AACTCTATGAAGAGTATCAAAGAGGAACCATTaGTCAACTTTTAGAGCAT
ATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGtTGATGGTAA
GAGAGATaCCGAGCGAGTGAAAGACAGTAGCCAACAGATCCACTAGTAT
TAGTAA

SEQ ID NO. 7411

STRAIN JM9130013

GAAATGCAAGTTCAAAAAAGTTTAAATCAAATACACATTACGGGA
CACTCTATCTAGTCCCACTCCAATTGGTAATCTAGATGATATGACTTTT
CGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTGTGTCAGAGGATAC
ACGAAATACGGGACTTTTACTCAAGCCTTTGATATTACTACTAAACAA
TTGATTTTACGAACACAATGCTTATGATAAAATCTCTGGGTTAATTGAT
TTGTTAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGGAATGCC
CTCTATTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGG
ATATCCCGGTCGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTC
ATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTATGGCTTCTTACC
GCGTAAGCAAGTCAACAAATAACTTTTGTGAAACAAGAAAGATTACC
CTGAAACACAATCTTTTATGAGTACCGTTCGAGTCTCTGATACGCTA
AAACACATGAAGAGATTTATGGAGATCGCCAAGTTGTTTATGACGCGA
ATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCACTTT
TAGGGCATATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTT
GATGGTAAGAGAGATACTAGCGAGTGAAAGACAGTAGCCAACAGATCC
AGTAGTATTAGTAA

PRETTY of: /biotmp/msa323014.2{*} March 28, 2003 02:40 ..

	1		50
msa323014.2{343_18RS21}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA
msa323014.2{343_A909}	-----	-AGTTCAAAA	AAGTTTTAAA
msa323014.2{343_COH1}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA
msa323014.2{343_M732}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA
msa323014.2{343_M781}	---aaatgc	aAGTTCAAAA	AAGTTTTAAA
msa323014.2{343_2603}	atggaaatgc	aAGTTCAAAA	AAGTTTTAAA
msa323014.2{343_1169NT}	-----	atgc	aAGTTCAAAA
msa323014.2{343_090}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA
msa323014.2{343_CJB110}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA
msa323014.2{343_H36B}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA
msa323014.2{343_JM9130013}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA
Consensus	*****	*****	*****

	51		100
msa323014.2{343_18RS21}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_A909}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_COH1}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_M732}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_M781}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_2603}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_1169NT}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_090}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_CJB110}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_H36B}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_JM9130013}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
Consensus	*****	*****	*****

	101		150
msa323014.2{343_18RS21}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT
msa323014.2{343_A909}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT
msa323014.2{343_COH1}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT
msa323014.2{343_M732}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT
msa323014.2{343_M781}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT
msa323014.2{343_2603}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT
msa323014.2{343_1169NT}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT
msa323014.2{343_090}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT

Table 74: Comparative Sequences relating to SAG1572

msa323014.2{343_CJB110}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT	TTATTGTGTC	AGAGGATACA
msa323014.2{343_H36B}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT	TTATTGTGTC	AGAGGATACA
msa323014.2{343_JM9130013}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT	TTATTGTGTC	AGAGGATACA
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	151				200
msa323014.2{343_A909}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_COH1}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_M732}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_M781}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_2603}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_1169NT}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_090}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_CJB110}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_H36B}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_JM9130013}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	201				250
msa323014.2{343_A909}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_COH1}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_M732}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_M781}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_2603}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_1169NT}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_090}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_CJB110}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_H36B}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_JM9130013}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	251				300
msa323014.2{343_A909}	TGTTAAAAGA	AGGGGaaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_COH1}	TGTTAAAAGA	AGGGGaaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_M732}	TGTTAAAAGA	AGGGGaaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_M781}	TGTTAAAAGA	AGGGGaaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_2603}	TGTTAAAAGA	AGGGGaaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_1169NT}	TGTTAAAAGA	AGGGGaaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_090}	TGTTAAAAGA	AGGGGaaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_CJB110}	TGTTAAAAGA	AGGGGaaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_H36B}	TGTTAAAAGA	AGGGGaaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_JM9130013}	TGTTAAAAGA	AGGGGaaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	301				350
msa323014.2{343_A909}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_COH1}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_M732}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_M781}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_2603}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_1169NT}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_090}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_CJB110}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_H36B}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_JM9130013}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	351				400
msa323014.2{343_A909}	tATCCCaGtT	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_COH1}	tATCCCaGtT	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_M732}	tATCCCaGtT	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_M781}	tATCCCaGtT	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_2603}	tATCCCaGtT	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_1169NT}	tATCCCaGtT	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_090}	gATCCCGtTc	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_CJB110}	gATCCCGtTc	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_H36B}	tATCCCGtTc	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_JM9130013}	tATCCCGtTc	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	401				450
msa323014.2{343_A909}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_COH1}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_M732}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_M781}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_2603}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_1169NT}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa

Table 74: Comparative Sequences relating to SAG1572

msa323014.2{343_090}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCg		
msa323014.2{343_CJB110}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCg		
msa323014.2{343_H36B}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCg		
msa323014.2{343_JM9130013}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCg		
Consensus	*****	*****	*****	*****	*****-		
msa323014.2{343_18RS21}	451	CGTAAGaAAG	GTCAACAAAT	AACITTTcTTT	GAAACAAAGc	AAGATTacCC	500
msa323014.2{343_A909}	CGTAAGaAAG	GTCAACAAAT	AACITTTcTTT	GAAACAAAGc	AAGATTacCC		
msa323014.2{343_COH1}	CGTAAGaAAG	GTCAACAAAT	AACITTTcTTT	GAAACAAAGc	AAGATTacCC		
msa323014.2{343_M732}	CGTAAGaAAG	GTCAACAAAT	AACITTTcTTT	GAAACAAAGc	AAGATTacCC		
msa323014.2{343_M781}	CGTAAGaAAG	GTCAACAAAT	AACITTTcTTT	GAAACAAAGc	AAGATTacCC		
msa323014.2{343_2603}	CGTAAGaAAG	GTCAACAAAT	AACITTTcTTT	GAAACAAAGc	AAGATTacCC		
msa323014.2{343_1169NT}	CGTAAGaAAG	GTCAACAAAT	AACITTTcTTT	GAAACAAAGc	AAGATTacCC		
msa323014.2{343_090}	CGTAAGaAAG	GTCAACAAAT	AACITTTcTTT	GAAACAAAGc	AAGATTacCC		
msa323014.2{343_CJB110}	CGTAAGaAAG	GTCAACAAAT	AACITTTcTTT	GAAACAAAGc	AAGATTacCC		
msa323014.2{343_H36B}	CGTAAGcAAG	GTCAACAAAT	AACITTTcTTT	GAAACAAAGc	AAGATTacCC		
msa323014.2{343_JM9130013}	CGTAAGcAAG	GTCAACAAAT	AACITTTcTTT	GAAACAAAGc	AAGATTacCC		
Consensus	*****-***	*****	*****-***	*****	*****	*****-***	
msa323014.2{343_18RS21}	501	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA	550
msa323014.2{343_A909}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA		
msa323014.2{343_COH1}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA		
msa323014.2{343_M732}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA		
msa323014.2{343_M781}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA		
msa323014.2{343_2603}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA		
msa323014.2{343_1169NT}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA		
msa323014.2{343_090}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA		
msa323014.2{343_CJB110}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA		
msa323014.2{343_H36B}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA		
msa323014.2{343_JM9130013}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA		
Consensus	*****	*****	*****	*****	*****	*****	
msa323014.2{343_18RS21}	551	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA	600
msa323014.2{343_A909}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA		
msa323014.2{343_COH1}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA		
msa323014.2{343_M732}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA		
msa323014.2{343_M781}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA		
msa323014.2{343_2603}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA		
msa323014.2{343_1169NT}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA		
msa323014.2{343_090}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA		
msa323014.2{343_CJB110}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA		
msa323014.2{343_H36B}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA		
msa323014.2{343_JM9130013}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA		
Consensus	*****	*****	*****	*****	*****	*****	
msa323014.2{343_18RS21}	601	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTa	GTCAACTTTT	650
msa323014.2{343_A909}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTa	GTCAACTTTT		
msa323014.2{343_COH1}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTa	GTCAACTTTT		
msa323014.2{343_M732}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTa	GTCAACTTTT		
msa323014.2{343_M781}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTa	GTCAACTTTT		
msa323014.2{343_2603}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTa	GTCAACTTTT		
msa323014.2{343_1169NT}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTa	GTCAACTTTT		
msa323014.2{343_090}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTa	GTCAACTTTT		
msa323014.2{343_CJB110}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTa	GTCAACTTTT		
msa323014.2{343_H36B}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTa	GTCAACTTTT		
msa323014.2{343_JM9130013}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTa	GTCAACTTTT		
Consensus	*****	*****	*****	*****	*****	*****	
msa323014.2{343_18RS21}	651	AGaGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG	700
msa323014.2{343_A909}	AGaGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG		
msa323014.2{343_COH1}	AGaGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG		
msa323014.2{343_M732}	AGaGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG		
msa323014.2{343_M781}	AGaGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG		
msa323014.2{343_2603}	AGaGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG		
msa323014.2{343_1169NT}	AGaGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG		
msa323014.2{343_090}	AGgGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG		
msa323014.2{343_CJB110}	AGgGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG		
msa323014.2{343_H36B}	AGgGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG		
msa323014.2{343_JM9130013}	AGgGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG		
Consensus	**..*****	*****-****	*****	*****	*****	*****	
msa323014.2{343_18RS21}	701	ATGGTAAGAG	AGATACcGAG	CGAGTGAAG	ACAGTAGCCA	ACAAGATCCA	750
msa323014.2{343_A909}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAG	ACAGTAGCCA	ACAAGATCCA		
msa323014.2{343_COH1}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAG	ACAGTAGCCA	ACAAGATCCA		
msa323014.2{343_M732}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAG	ACAGTAGCCA	ACAAGATCCA		
msa323014.2{343_M781}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAG	ACAGTAGCCA	ACAAGATCCA		
msa323014.2{343_2603}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAG	ACAGTAGCCA	ACAAGATCCA		

Table 74: Comparative Sequences relating to SAG1572

msa323014.2{343_1169NT}	ATGGTAAGAG	AGATACCGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_090}	ATGGTAAGAG	AGATACCGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_CJB110}	ATGGTAAGAG	AGATACCGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_H36B}	ATGGTAAGAG	AGATACCGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_JM9130013}	ATGGTAAGAG	AGATACCGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
Consensus	*****	*****	*****	*****	*****
751					
msa323014.2{343_18RS21}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_A909}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_COH1}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_M732}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_M781}	cTAGTATTAG	TAAA-----	-----	-----	-----
msa323014.2{343_2603}	cTAGTATTAG	TAAAagaata	tatcgctaata	ggtgataaaa	ctaatacaagc
msa323014.2{343_1169NT}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_090}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_CJB110}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_H36B}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_JM9130013}	gTAGTATTAG	TAA-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
801					
msa323014.2{343_18RS21}	-----	-----	-----	-----	-----
msa323014.2{343_A909}	-----	-----	-----	-----	-----
msa323014.2{343_COH1}	-----	-----	-----	-----	-----
msa323014.2{343_M732}	-----	-----	-----	-----	-----
msa323014.2{343_M781}	-----	-----	-----	-----	-----
msa323014.2{343_2603}	gataaaaaaa	gtagcaaaaag	aatttaattct	caatagacaa	gaactctatg
msa323014.2{343_1169NT}	-----	-----	-----	-----	-----
msa323014.2{343_090}	-----	-----	-----	-----	-----
msa323014.2{343_CJB110}	-----	-----	-----	-----	-----
msa323014.2{343_H36B}	-----	-----	-----	-----	-----
msa323014.2{343_JM9130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
851					
msa323014.2{343_18RS21}	-----	-----	-----	-----	-----
msa323014.2{343_A909}	-----	-----	-----	-----	-----
msa323014.2{343_COH1}	-----	-----	-----	-----	-----
msa323014.2{343_M732}	-----	-----	-----	-----	-----
msa323014.2{343_M781}	-----	-----	-----	-----	-----
msa323014.2{343_2603}	ctagtttcca	tgattta	-----	-----	-----
msa323014.2{343_1169NT}	-----	-----	-----	-----	-----
msa323014.2{343_090}	-----	-----	-----	-----	-----
msa323014.2{343_CJB110}	-----	-----	-----	-----	-----
msa323014.2{343_H36B}	-----	-----	-----	-----	-----
msa323014.2{343_JM9130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	-----	-----	-----
851					
msa323014.2{343_18RS21}	-----	-----	-----	-----	-----
msa323014.2{343_A909}	-----	-----	-----	-----	-----
msa323014.2{343_COH1}	-----	-----	-----	-----	-----
msa323014.2{343_M732}	-----	-----	-----	-----	-----
msa323014.2{343_M781}	-----	-----	-----	-----	-----
msa323014.2{343_2603}	ctagtttcca	tgattta	-----	-----	-----
msa323014.2{343_1169NT}	-----	-----	-----	-----	-----
msa323014.2{343_090}	-----	-----	-----	-----	-----
msa323014.2{343_CJB110}	-----	-----	-----	-----	-----
msa323014.2{343_H36B}	-----	-----	-----	-----	-----
msa323014.2{343_JM9130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	-----	-----	-----

SEQ ID NO. 7412

STRAIN 2603 frame: 1

MEMQVQKSFKSNHYGTYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
 DITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPISIDPGHDLVKAAIEGDI
 PVVSIPGASAGITALIASGLAPQPHIFYGFLPRKKGQITFFETKQDYPETQIFYESPPFRVS
 DTLKHKMEIYGRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDT
 ERVKDSSQDPLVLV

SEQ ID NO. 7413

STRAIN 090 frame: 1

EMQVQKSFKSNHYGTYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
 ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPISIDPGHDLVKAAIEGDI
 PVVSIPGASAGITALIASGLAPQPHIFYGFLPRKKGQITFFETKQDYPETQIFYESPPFRVS
 DTLKHKMEIYGRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDT
 ERVKDSSQDPLVLV

SEQ ID NO. 7414

STRAIN A909 frame: 2

VQKSFKSNHYGTYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFDIT
 TTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPISIDPGHDLVKAAIEGDI
 PVVSIPGASAGITALIASGLAPQPHIFYGFLPRKKGQITFFETKQDYPETQIFYESPPFRVS
 DTLKHKMEIYGRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDT
 ERVKDSSQDPLVLV

SEQ ID NO. 7415

STRAIN H36B frame: 1

EMQVQKSFKSNHYGTYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
 ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPISIDPGHDLVKAAIEGDI
 PVVSIPGASAGITALIASGLAPQPHIFYGFLPRKKGQITFFETKQDYPETQIFYESPPFRVS
 DTLKHKMEIYGRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDT
 ERVKDSSQDPLVLV

SEQ ID NO. 7416

Table 74: Comparative Sequences relating to SAG1572

STRAIN 18RS21 frame: 1
 EMQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
 ITTKQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDTER
 VKDSSQDDPLVLV

SEQ ID NO. 7417

STRAIN M732 frame: 1
 EMQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
 ITTKQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDTER
 VKDSSQDDPLVLV

SEQ ID NO. 7418

STRAIN COH1 frame: 1
 EMQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
 ITTKQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDTER
 VKDSSQDDPLVLV

SEQ ID NO. 7419

STRAIN M781 frame: 3
 MQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFDI
 TTKQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVVS
 IPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSDT
 LKHMKEIYGRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDTERV
 KDSSQDDPLVLV

SEQ ID NO. 7420

STRAIN CJB110 frame: 1
 EMQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
 ITTKQISFHEHNAYDKISGLIDLKKEGRSLAQVSDAGMPSISDPGHDLVKAIEGGI PVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGRQVVLVRELTKLYEYQRTISQLLGHIEKVPLKGECLIIVDGKRDTER
 VKDSSQDDPLVLV

SEQ ID NO. 7421

STRAIN 1169NT frame: 3
 QVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFDIT
 TKQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVVSI
 PGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSDTL
 KHMKEIYGRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDTERVK
 DSSQDDPLVLV

SEQ ID NO. 7422

STRAIN JM9130013 frame: 1
 EMQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
 ITTKQISFHEHNAYDKISGLIDLKKEGRSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGRQVVLVRELTKLYEYQRTISQLLGHIEKVPLKGECLIIVDGKRDTER
 VKDSSQDDPVVLV

msa324064.2{343_18RS21}	1	50
msa324064.2{343_A909}	~emqVQKSFK SNIHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT	
msa324064.2{343_M781}	----VQKSFK SNIHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT	
msa324064.2{343_2603}	~mqVQKSFK SNIHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT	
msa324064.2{343_COH1}	memqVQKSFK SNIHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT	
msa324064.2{343_M732}	~emqVQKSFK SNIHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT	
msa324064.2{343_1169NT}	---qVQKSFK SNCHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT	
msa324064.2{343_090}	~emqVQKSFK SNCHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT	
msa324064.2{343_CJB110}	~emqVQKSFK SNCHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT	
msa324064.2{343_H36B}	~emqVQKSFK SNCHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT	
msa324064.2{343_JM9130013}	~emqVQKSFK SNCHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT	
Consensus	*--***** **-***** ***** ***** *****	
msa324064.2{343_18RS21}	51	100
msa324064.2{343_A909}	RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP	
msa324064.2{343_M781}	RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP	
msa324064.2{343_2603}	RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP	
msa324064.2{343_COH1}	RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP	
msa324064.2{343_M732}	RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP	
msa324064.2{343_1169NT}	RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP	
msa324064.2{343_090}	RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP	
msa324064.2{343_CJB110}	RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP	
msa324064.2{343_H36B}	RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP	
msa324064.2{343_JM9130013}	RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP	
Consensus	***** ***** ***** ***** *****	

Table 74: Comparative Sequences relating to SAG1572

	101				150
msa324064.2{343_18RS21}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_A909}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_M781}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_2603}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_COH1}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_M732}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_1169NT}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_090}	SISDPGHDLV	KAAIEGgIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_CJB110}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_H36B}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_JM9130013}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
Consensus	*****	*****_***	*****	*****	*****
	151				200
msa324064.2{343_18RS21}	RKkGQQITFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKIY	GDRQVVLVRE
msa324064.2{343_A909}	RKkGQQITFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKIY	GDRQVVLVRE
msa324064.2{343_M781}	RKkGQQITFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKIY	GDRQVVLVRE
msa324064.2{343_2603}	RKkGQQITFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKIY	GDRQVVLVRE
msa324064.2{343_COH1}	RKkGQQITFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKIY	GDRQVVLVRE
msa324064.2{343_M732}	RKkGQQITFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKIY	GDRQVVLVRE
msa324064.2{343_1169NT}	RKkGQQITFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKIY	GDRQVVLVRE
msa324064.2{343_090}	RKkGQQITFF	ETKkDYPETQ	IFYESPFRVS	DTLKHMKIY	GDRQVVLVRE
msa324064.2{343_CJB110}	RKkGQQITFF	ETKkDYPETQ	IFYESPFRVS	DTLKHMKIY	GDRQVVLVRE
msa324064.2{343_H36B}	RKkGQQITFF	ETKkDYPETQ	IFYESPFRVS	DTLKHMKIY	GDRQVVLVRE
msa324064.2{343_JM9130013}	RKkGQQITFF	ETKkDYPETQ	IFYESPFRVS	DTLKHMKIY	GDRQVVLVRE
Consensus	**_*****	***_*****	*****	*****	*****
	201				250
msa324064.2{343_18RS21}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_A909}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_M781}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_2603}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_COH1}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_M732}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_1169NT}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_090}	LTKLYEEYQR	GTISQLLgHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_CJB110}	LTKLYEEYQR	GTISQLLgHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_H36B}	LTKLYEEYQR	GTISQLLgHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_JM9130013}	LTKLYEEYQR	GTISQLLgHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
Consensus	*****	*****_**	*****	*****	*****
	251				289
msa324064.2{343_18RS21}	LVLV-----	-----	-----	-----	-----
msa324064.2{343_A909}	LVLV-----	-----	-----	-----	-----
msa324064.2{343_M781}	LVLV-----	-----	-----	-----	-----
msa324064.2{343_2603}	LVLVkeyian	gdktngaiikk	vakefnlnrq	elyasfhdI	-----
msa324064.2{343_COH1}	LVLV-----	-----	-----	-----	-----
msa324064.2{343_M732}	LVLV-----	-----	-----	-----	-----
msa324064.2{343_1169NT}	LVLV-----	-----	-----	-----	-----
msa324064.2{343_090}	LVLV-----	-----	-----	-----	-----
msa324064.2{343_CJB110}	LVLV-----	-----	-----	-----	-----
msa324064.2{343_H36B}	LVLV-----	-----	-----	-----	-----
msa324064.2{343_JM9130013}	vVLV-----	-----	-----	-----	-----
Consensus	-*****	*****	*****	*****	*****

Table 75: Comparative Sequences relating to SAG0671

SEQ ID NO. 7501
STRAIN 2603
ATGAGCGTATATGTTAGTGGGAATAGGAATTATT
TCTTCTTTGGGAAAGAATTATAGCGAGCATAAACAGCATCTCTTCGACTTAAAGAAGGA
ATTTCTAAACATTTATATAAAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATA
ACTAGTGACCCAGAGGTTCTCTGAGCAATACAAAGATGAGACACGTAATTTAAATTTGCT
TTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTTAAAGCTTATCATAT
ATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAAAGAGTGTGGTCAAATGCCTTGTAT
CAATTTGAAGAAGGAGAGCGTCAAGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTAC
CATATTGCTGATGAATTTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTC
ACCGCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAAGATGGC
GATTGTGATTTAGCTATTTTGGTGGCTGTGATGAGTTAAGTGATATTTCTTTAGCAGGC
TTCACATCACTAGGAGCTATTAATACAGAAATGGCATGTGAGCCCTATTCTCTGGAAAA
GGAATCAATTTGGGTGAGGGCGCTGGTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCT
AAATATGAAAAATTATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCT
AAGCCAACAGGTGAAGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCAGGTATT
GACTACAGTGAGATTGACTATATTAAACGGTCACGGTACAGGTACTCAAGCTAATGATAAA
ATGGAAAAAATATGATGTTAAGTTTTCGCCACAACGACATTGATCAGCAGTACCAAG
GGGCAACGGGTCATACCTCTAGGGGCTGCAGGTATTATCGAATTGATTAAATGTTTAGCG
GCAATAGAGGAACAGACTGTACCAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCA
GAAAAATTTGTCTATCATCAAAGAGAGAATACCCAAATAAGAAATGCTTTAAATTTTTCG
TTTGTCTTTGGTGGAAATAATAGTGGTGTCTTATTGTCATCTTTAGATTCACTCTAGAA
ACATTACCTGCTAGAGAAAAATCTTAAATGGCTATCTTATCATCTGTGCTTCCATTCT
AAGAATGAATCAGTTCTTCTATAACCTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAA
GCATTACGCTTTTAAAGGGGCTAGACCACCAAACTGTCAACCCAGCACAAATTTAGGAAA
ATGATGATTTTTCCAAAATGGTTGCCGTAAACAGCTCAAGCACTAATAGAAAGCAAT
ATTAATCTAAAAAACAAGATACTTCAAAGTAGGAATTTGATTTACAACACTTTCTGGA
CCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAATCAACAAGAGGATATGCACATGTT
TCTGCTTCAGCATTCCTGTTTACGTAATGAATGCAGCAGCTGGTATGCTTTCTATCATT
TTTAAAAATAACAGGTCTTTTATCTGTCTTTTCGACAAATAGTGGAGCGCTTGATGGTATA
CAATATGCCAAGGAATGATCGCTAACGATAATCTAGACTATGTGATTCTTGTCTCTGCT
AATCAGTGGGACAGACAGATTTTATGTGGTGGCAACAATTAACATATGATAGTCAAATG
TTTGTGCTTCTGATTATTGTTTCAGCACAAAGTCTCTCTCGTCAAGCATTTGGATAATTCT
CCTATAATATTAGGTAGTAAACAATTAATATAGCCATAAAACATTACAGATGTGATG
ACTATTTTGTGCTGCTGCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAAGAT
ATCAAAGGTTTCTGTTTGAATGAGCGGAAGAGGAGGAGTTAGTTTCAAGATTGATTTCTTA
GCGAATCTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTGGTCAGTTTGGATTTTCA
TCTAATGCTGCTGGTGAAGAAGTGGACTATAGTTAATGAAAGTATAGAAAAGGCTAT
TATTAGTCTATCTTATCGATCTTCGGTGGTATCTCTTTGTCTATTATTGAAAAAGG

SEQ ID NO. 7502
STRAIN 090
ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGaATTAT
AGCGAGCATAAACAGCATCTCTTCGACTTAAAGAAGGAATTTCTAAACA
TTTATATAAAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATAA
CTAGTGACCCAGAGGTTCTCTGAGCAATACAAAGATGAGACACGTAATTTT
AAATTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAA
TTTAAAGCTTTATCATAATATGCTGTGTGTTTAGGGACCTCACTTGGGG
GAAAGAGTGTGCTCAAATGCCCTGTATCAATTTGAAGAAGGAGAGCGT
CAAGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGA
TGAATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAA
CCGCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTAATT
CAAGATGGCGAATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAG
TGATATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAATACAGAAA
TGGCATGTGAGCCCTATTCTTCTGAAAAAGGAATCAATTTGGGTGAGGGC
GCTGGTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCTAATATGGA
AATTATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTA
AGCCAACAGGTGAAGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAA
GCAGGTATTGACTACAGTGAGATTGACTATATTAAACGGTCACGGTACAGG
TACTCAAGCTAATGATAAAATGGAAGAAAAATATGATGGTAAGTTTTC
CGACAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCACTCTA
GGGGCTGCAGGTATTATCGAATTGATTAAATGTTTAGCGGCAATAGAGGA
ACAGACTGTACCAGCACTAAAAATGAGATTGGGATAGAAGGTTTTCCAG
AAAAATTTGTCTATCATCAAAGAGAGAATACCCAATAAGAAATGCTTTA
AATTTTCTGTTTGTCTTTGGTGGAAATAATAGTGGTATCTTATTGTCTATC
TTTAGATTCACTCTAGAAACATTACCTGCTAGAGAAAATCTTAAATG
CTATCTTATCATCTGTGCTTCCATTCTAAGAAATGAATCACTTTCTATA
ACCTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTT
TAAAGGGGCTAGACCACCAAACTGTCAACCCAGCACAATTTAGGAAAA
TGGATGATTTTCCAAAATGGTTGCCGTAAACAAGCTCAAGCACTAATA
GAAAGCAATATTAACTAAAAAACAAGTACTTCAAAGTAGGAATGTT
ATTTACAACACTTTCTGGACCAAGTTGAGGTTGTTGAAGGTATTGAAAGC
AAATCACAACAGAGGATATGCACATGTTTCTGCTTCAGGATTCCTGTTT
ACAGTAATGAATGCAGCAGCTGGTATGCTTCTATCATTTTAAAAATAAC
AGGTCCTTTATCTGCTATTTGACAAATAGTGGAGCGCTTGATGGTATAC
AATATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTT
GTTTCTGCTAATCAGTGACAGACATGAGTTTATGTGGTGGCAACAAAT
AAACTATGATAGTCAAATGTTTGTGCGTTCTGATTATTGTTTCAGCACAAG
TCCTCTCTGCTCAAGCATTTGGATAATTCTCTATAATATTAGGTAGTAAA
CAATTAAAAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGA
TGCTGCGCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAAGATA
TCAAAGGTTTCTGTTTGAATGAGCGGAAGAGGAGTTAGTTAGATTAT
GATTTCTTAGCGAATCTGTGAGTATTATAATATGCCAAACCTTGCTTC

Table 75: Comparative Sequences relating to SAG0671

TGGTCAGTTTGGATTTTCATCTAATGGTGTGGTGAAGAACTGGACTATA
CTGTTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTCTATTTCG
ATCTTTGGTGGTATCTCTTTTGTCTATTATTGAAAAAAGG

SEQ ID NO. 7503

STRAIN A909

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATT
ATAGCGAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAA
CATTTATATATAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCAT
AACTAGTGACCCAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAATT
TTAAATTTGCTTTTACCCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTT
AATTTAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGG
GGGAAAGAGTGCTGGTCAAAATGCCCTTGATCAATTTGAAGAAGGAGAGC
GTCAAGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCT
GATGAATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTT
AACCCGCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTAC
TTCAGAGATGGCGATTGTGATTAGCTATTGTGGTGGCTGTGATGAGTTA
AGTGATATTCTTTAGCAGGCTTCAATCACTAGGAGCTATTAATACAGA
AATGGCATGTGAGCCCTATTCTTCTGAAAAGGAATCAATTTGGGTGAGG
GCGCTGGTTTGTGTTCTTGTCAAAGATCAGTCTTCTAGCTAAATATGGA
AAAATTATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACC
TAAGCCAACAGGTGAAGGGGCGGCACAGATTGCAAGCAGCTAGTGACTC
AAGCAGGTATTGACTACAGTGAGATTGACTATATTAAACGGTCACGGTACA
GGTACTCAAGCTAATGATAAAATGGAATAATATGTTATGTTAAGTTT
CCCGACAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCTACTC
TAGGGGCTGACAGTATTATCGAATTGATTAAATTGTTTAGCGGCAATAGAG
GAACAGACTGTACAGCAACTAAAAATGAGATTGGGATAGAAGGTTTCC
AGAAAATTTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTT
TAAATTTTTCGTTTGTCTTTTGGTGAATAATAGTGGTGTCTTATTGTCA
TCTTTAGATTCACTCTAGAAAACATTACCTGCTAGAGAAAAATCTTAAAT
GGCTATCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTA
TAACCTATTGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGC
TTTAAAGGGGCTAGACCAACCAAACTGTCAACCCAGCACATTTAGGAA
AATGGATGATTTTCCAAAATGGTTGCCGTAAACAGCTCAAGCACTAA
TAGAAAGCAATAATTAATCTAAAAAACAAGATACTTCAAAAGTAGGAATT
GTATTTACAAACATTTCTGACCAGTTGAGGTTGTTGAAGGTATTGAAAA
GCAAAATCAACAACGAAGGATATGCATGTTTCTGCTTACAGATTCCCGT
TTACAGTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTAAATA
ACAGGTCCTTTATCTGTCTATTTCGACAAATAGTGGAGCGCTTGATGGTAT
ACAAATATGCAAGGAAATGATGCGTAAACGATAATCTAGACTATGTGATTC
TTGTTTCTGCTAATCAGTGGACAGACATGAGTTTATGTGTGGCAACA
TTAACTATGATAGTCAAAATGTTTGTCCGTTCTGATTATTGTTCAACACA
AGTCTCTCTCTCGTCAAGCATTGGATAAATCTCTATAATATTAGGTAGTA
AACAAATAAATATAGCCATAAAACATTACAGATGTGATGACTATTTTT
GATGCTGCGCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAGA
TATCAAGGTTTTCGTTTGAAGTGAAGCGGAAGGACAGTTAGTTCAAGATT
ATGATTTCTTAGCGAACTTGTCTGAGTATTATATATGCCAAACCTTGCT
TCTGGTCAGTTTGGATTTCATCTAATGGTGTCTGGTGAAGAACTGGACTA
TACTGTTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTCTATCTTATT
CGATCTTCGGTGTATCTCTTTTGTCTATTATTGAAAAAAGG

SEQ ID NO. 7504

STRAIN H36B

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGCGA
GCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATTAT
ATAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCATAACTAGT
GACCCAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAATTTTAAATT
TGCTTTTACCCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTTAA
AAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAAAG
AGTGCTGGTCAAAATGCCCTTGATCAATTTGAAGAAGGAGAGCGTCAAGT
AGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATGAAT
TGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCGCC
TGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAAGA
TGGCGATTGTGATTAGCTATTGTGGTGGCTGTGATGAGTTAAGTGATA
TTTCTTTAGCAGGCTTCAATCACTAGGAGCTATTAATACAGAAATGGCA
TGTCAGCCCTATTCTTCTGAAAAGGAATCAATTTGGGTGAGGGCGCTGG
TTTTGTGTTCTTGTCAAAGATCAGTCTTCTAGCTAAATATGGAATAATTA
TCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAGCCA
ACAGGTGAAGGGGCGGCACAGATTGCAAGCAGCTAGTGACTCAAGCAGG
TATTGACTACAGTGAGATTGACTATATTAAACGGTCACGGTACAGGTACTC
AAGCTAATGATAAAATGGAATAAATATGTTATGTTAAGTTTTCCTGACA
ACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCTACTCTAGGGGC
TGCAGGTATTATCGAATTGATTAAATTGTTTAGCGGCAATAGAGGAACAGA
CTGTACCAAGCAACTAAAAATGAGATTGGGATAGAAGGTTTCCAGAAAAAT
TTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAATTT
TTCGTTTGTCTTTGGTGAATAAATAGTGGTGTCTTATTGTCTATCTTTAG
ATTCACTCTAGAAAAATTACCTGCTAGAGAAAAATCTTAAATGGCTATC
TTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACCTA
TGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAAAG
GGGCTAGACCAACCAAACTGTCAACCCAGCACAAATTTAGGAAAAATGGAT
GATTTTTCAAAAATGGTTGCCGTAAACAGCTCAAGCACTAATAGAAAG
CAATATTAACTCAAAAAAACAAGATACTTCAAAAGTAGGAATTGTATTTA
CAACACTTTCTGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAATC

Table 75: Comparative Sequences relating to SAG0671

ACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCCGTTTACAGT
AATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTAAAAATAACAGGTC
CTTTATCTGTCTATTTCCGACAAATAGTGGAGCGCTTGATGGTATACAAATAT
GCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCCTGTTTT
TGCTAATCAGTGGACAGACATGAGTTTTATGTGGTGGCAACAATTAACCT
ATGATAGTCAAAATGTTTGTGCGTTCTGATTATTGTTCCAGCACAAGTCCTC
TCTCGTCAAGCATTTGGATAATTCTCTATAATATTAGGTAGTAAACAATT
AAAAATATAGCCATAAAACATTACAGATGTGATGACTATTTTTGATGCTG
CGCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATCAAA
GGTTTCGTTTGAAGTGAAGCGGAAGAGGAGGAGTTAGTTTATGATTTT
CTTAGCGAATCTGTCTGAGTATTATAATATGCCAACCTTGCTTCTGGTC
AGTTTGGATTTTCATCTAATGGTGTGCTGGTGAAGAACTGGACTATCTGTT
AATGAAAGTATAGAAAAGGGCTATTATTAGTCTTATTCGATCTT
CGGTGGTATCTCTTTTGTCTATTATTGAAAAAAGG

SEQ ID NO. 7505

STRAIN 18RS21

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGC
GAGCATAAACAGCATCTCTTCGACTTAAAGAAGGAATTTCTAAACATTT
ATATAAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATAACTA
GTGACCCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATTTTAA
TTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTT
AAAAGCTTATCATAATATTGCTGTGTGTTAGGGACCTCAGTTGGGGGA
AGAGTGTGCTGCTCAAAATGCTTGTATCAATTTGAAGAAGGAGAGCGTCAA
GTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATGA
ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCG
CCTGTTCTGCAAGTAATAATGCGTAATAATTAGGAACACAATTACTTCAA
GATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGA
TATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAAATACAGAAATGG
CATGTCAGCCCTATTCTTCTGGAAGGAATCAATTTGGGTGAGGGCGCT
GGTTTGTGTTCTTGTCAAAGATCAGTCCCTAGCTAAATATGGAAGAAAT
TATCGGTGCTTATTACTTTCAGATGGTTATCATATAACAGCACCTTAAGC
CAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCA
GGTATTGACTACAGTGAGATTGACTATTTAAACGGTACCGGTACAGGTAC
TCAAGCTAATGATAAAATGGAAGAAATATGTATGGTAAGTTTTCCTCGA
CAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCTACTCTAGGG
GCTGCAAGTATTATCGAATTGATTAAATGTTTACGGCAATAGAGGAACA
GACTGTACAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCAGAAA
ATTTTGTCTATCATCAAAAGAGAGAAATACCAATAAGAAATGCTTTAAAT
TTTTGCTTTGCTTTTGGTGAATAATAGTGGTGTCTTATTGTCTATCTTT
AGATTACCTCTAGAAACATTACCTGCTAGAGAAATCTTAAATGGCTA
TCTTATCATCTGTGCTTCCATTTCTAAGAAATGAATCACTTTCTATAACC
TATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
AGGGGCTAGACCCCAAACTGTCAACCCAGCACAATTTAGGAAATGG
ATGATTTTTCCAAATGGTTGCGGTAACAACAGCTCAAGCACTAATAGAA
AGCAATATTAACTTAAAAAACAAGTACTTCAAAAGTAGGAATTGTATT
TACAACACTTTCTGGACAGTTGAGGTTGTTGAAGGTATTGAAAAGCAAA
TCACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCGTTTACA
GTAATGAATGCAAGCTGGTATGCTTTCTATCATTTTAAATAACAGG
TCCTTTATCTGTCTTTTCGACAAATAGTGGAGCGCTTGATGGTATACAAT
ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGTT
TCTGTCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTA
CTATGATGATCAAAATGTTTGTGCGTTCTGATTATTGTTTCAGCACAAGTCC
TCTCTCGTCAAGCATTGGATAATTCTCTATAATATTAGGTAGTAAACAA
TTAAATATATAGCCATAAAACATTACAGATGTGATGACTATTTTTGATGC
TGCGCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATCA
AAGGTTTCGTTTGAAGTGAAGCGGAAGAGGAGTTAGTTTATGATTTATGAT
TTCTTAGCGAATCTGTCTGAGTATTATAATATGCCAACCTTGCTTCTGG
TCAGTTTGGATTTTTCATCTAATGGTGTGCTGGTGAAGAACTGGACTATCTG
TTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTTATCTTATTCGATC
TTCGGTGGTATCTCTTTTGTCTATTATTGAAAAAAGG

SEQ ID NO. 7506

STRAIN M732

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAG
CGAGCATAAACAGCATCTCTTCGACTTAAAGAAGGAATTTCTAAACATT
TATATAAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATAACT
AGTGACCCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATTTTAA
ATTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTT
TAAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCAGTTGGGGGA
AAGAGTGTGCTGCTCAAAATGCTTGTATCAATTTGAAGAAGGAGAGCGTCA
AGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATG
AATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACC
GCCTGTTCTGCAAGTAATAATGCCGTAATAATTAGGAACACAATTACTTCA
AGATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTG
ATATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAAATACAGAAATG
GCATGTCAGCCCTATTCTTCTGGAAGGAATCAATTTGGGTGAGGGCGC
TGGTTTTGTGTTCTTGTCAAAGATCAGTCCCTAGCTAAATATGGAAGAA
TTATCGGTGGTCTTATTACTTTCAGATGGTTATCATATAACAGCACCTAAG
CCAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGC
AGGTATTGACTACAGTGAGATTGACTATTTAAACGGTACCGGTACAGGTA
CTCAAGCTAATGATAAAATGGAAGAAATATGTATGGTAAGTTTTCCTCG
ACAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCTACTCTAGG

Table 75: Comparative Sequences relating to SAG0671

GGCTGCAGGTATTATCGAATTGATTAATTGTTTAGCGGCAATAGAGGAAC
 AGACTGTACCAGCACTAAAAATGAGATTGGGATAGAAGGTTTCCAGAA
 AATTTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAA
 TTTTTCGTTTGGCTTTGGTGGAAATAATAGTGGTGTCTTATTGTCATCT
 TAGATTACCTCTAGAAAACATTACCTGCTAGAGAAAATCTTAAATGGCT
 ATCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAAC
 CTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTA
 AAGGGGCTAGACCACCCAAAACCTGTCAACCCAGCACAATTTAGGAAAATG
 GATGATTTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGA
 AAGCAATATTAATCTAAAAAACAAGATACTTCAAAGTAGGAATTGTAT
 TTACAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAA
 ATCACAACAGAAGGATATGCACATGTTTCTGCTTCAAGATTCCCGTTTAC
 AGTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTAAATAACAG
 GTCCTTTATCTGTCATTTTCGACAAATAGTGGAGCGCTTGATGGTATACAA
 TATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGT
 TTCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTAA
 ACTATGATAGTCAAAATGTTTGTGCGTTCTGATTATTGTTCAAGCAAGTC
 CTCTCTCGTCAAGCATTGGATAATTCTCTATAATATTAGGTAGTAAACA
 ATTAAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGGATG
 CTGCGCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATC
 AAAGGTTTCGTTTGAATGAGCGGAAGAAGGCAGTTAGTTCAAGATTATGA
 TTTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTG
 GTCAGTTTGGATTTCATCTAATGGTGTGCTGGAAGAACTGGACTataCT
 GTTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTCTATCTTATTCGAT
 CTTCCGGTGGTATCTCTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7507

STRAIN COH1

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGC
 GAGCATAAACAGCATCTCTTCGACTTAAAGAAGGAATTTCTAAACATT
 ATATAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATAACTA
 GTGACCAGAGGTTCTGAGCAATACAAGATGAGACACGTAATTTTAAA
 TTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATT
 AAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAA
 AGAGTGTGGTCAAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCAA
 GTAGATGCTAGTTTATTAGAAAAGCATCTGTTTACCATATTGCTGATGA
 ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTCAACCG
 CCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAA
 GATGGCGATTGTGATTAGCTATTGTGGTGGCTGTGATGAGTTAAGTGA
 TATTTCTTTTAGCAGGCTTCACTCACTAGGAGCTATTAATACAGAAATGG
 CATGTCCAGCCCTATTCTCTGGAAGGAATCAATTGGGTGAGGGCGCT
 GGTTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGAAAAAT
 TATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAGC
 CAAAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCA
 GGTATTGACTACAGTGAGATTGACTATATTACCGTCACGGTACAGGTAC
 TCAAGCTAATGATAAAATGAAAAAATATGTATGGTAAGTTTTCCTCGA
 CAACGACATTGATCAGCAGTACCAAGGGGCAAACGGGTCTACTCTAGGG
 GCTGCAAGTATTATCGAATTGATTAAATTGTTTAGCGGCAATAGAGGAACA
 GACTGTACCAGCACTAAAAATGAGATTGGGATAGAAGGTTTTCAGAAA
 ATTTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAAT
 TTTTCGTTTGGCTTTTGGTGGAAATAATAGTGGTGTCTTATTGTCATCTT
 AGATTACCTCTAGAAAACATTACCTGCTAGAGAAAATCTTAAATGGCTA
 TCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACC
 TATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
 AGGGGCTAGACCACCCAAAACCTGTCAACCCAGCACAATTTAGGAAAATGG
 ATGATTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAA
 AGCAATATTAATCTAAAAAACAAGATACTTCAAAGTAGGAATTGTATT
 TACAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAAA
 TCACAACAGAAGGATATGCACATGTTTCTGCTTCAAGATTCCCGTTTACA
 GTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTAAATAACAGG
 TCCCTTTATCTGTCATTTTCGACAAATAGTGGAGCGCTTGATGGTATACAA
 ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGT
 TCTGTCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTAA
 CTATGATAGTCAAAATGTTTGTGCGTTCTGATTATTGTTCAAGCAAGTCC
 TCTCTCGTCAAGCATTGGATAATTCTCTATAATATTAGGTAGTAAACAA
 TTAATAATAGCCATAAAACATTACAGATGTGATGACTATTTTGTGTC
 TGGCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATCA
 AAGGTTTCGTTTGAATGAGCGGAAGAAGGCAGTTAGTTCAAGATTATGAT
 TTTCTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTGG
 TCAGTTTGGATTTCATCTAATGGTGTGCTGGAAGAACTGGACTATCTG
 TTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTCTATCTTATTCGATC
 TTCCGGTGGTATCTCTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7508

STRAIN M781

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGC
 GAGCATAAACAGCATCTCTTCGACTTAAAGAAGGAATTTCTAAACATT
 ATATAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATAACTA
 GTGACCAGAGGTTCTGAGCAATACAAGATGAGACACGTAATTTTAAA
 TTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATT
 AAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAA
 AGAGTGTGGTCAAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCAA
 GTAGATGCTAGTTATTAGAAAAGCATCTGTTTACCATATTGCTGATGA

Table 75: Comparative Sequences relating to SAG0671

ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCG
 CCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAA
 GATGGCGATTGTGATTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGA
 TATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAATACAGAAATGG
 CATGTACAGCCCTATTCTCTGGAAAAGGAATCAATTTGGGTGAGGGCGCT
 GGTTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAATAAT
 TATCGGTGGTCTTATTAATCTCAGATGGTTATCATATAACAGCACCTAAGC
 CAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCA
 GGTATTGACTACAGTGAGATTGACTATATTAATGGTCACGGTACAGGTAC
 TCAAGCTAATGATAAAATGGAATAAATATGTATGGTAAGTTTTCCCGA
 CAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTACATACTCTAGGG
 GCTGCAGGTATTATCGAATTGATTAAATGTTTGTAGCGCAATAGAGGAACA
 GACTGTACAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCAGAAA
 ATTTTGTCTATCATCAAAAGAGAGAATACCAATAAGAAATGCTTTAAAT
 TTTTCGTTTGTCTTTTGGTGGAAATAATAGTGGTATCTTATTGTCACTTT
 AGATTCACTCTAGAAAACATTACCTGTAGAGAAAATCTTAAATGGCTA
 TCTTATCATCTGTTGCTTCCATTCTAAGAATGAATCACTTCTATAACC
 TATGAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
 AGGGGCTAGACCACCCAAAACCTGTCAACCCAGCACAAATTTAGGAAAATGG
 ATGATTTTCCAAAATGGTTGCCGTAACCAACAGCTCAAGCACTAATAGAA
 AGCAATATTAATCTAAAAAACAAGATACTTCAAAGTAGGAATGTATT
 TACAACACTTTCTGGACCGTTGAGGTTGTGAAGGTATTGAAAAGCAAA
 TCACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCTCGTTTACA
 GTAATGAATGCAGCAGCTGGTATGCTTCTATCATTTTAAATAACAGG
 TCCCTTATCTGTCACTTCGACAAATAGTGGAGCGCTTGATGGTATACAAT
 ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTGTGT
 TCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTAA
 CTATGATAGTCAAATGTTTGTGCGTTCTGATTATTGTTTCAACAGTCC
 TCTCTCGTCAAGCATTGGGATAATCTCCTATAATATTAGGTAGTAAACAA
 TTAATAATATAGCCATAAAACATTCAAGATGTGATGACTATTTTGTATGC
 TGGCCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAGATATCA
 AAGGTTTCGTTTGGAAATGAGCGGAAGAAGGCAGTTAGTTTCAAGTTATGAT
 TTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGTCTCTGG
 TCAGTTTGGATTTCATCTAATGGTGTGGTGAAGAACTGGACTATACTG
 TTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTCTATCTATTTCGATC
 TTTGGTGGTATCTCTTTTGTCTATTATTGAAAAAAGG

SEQ ID NO. 7509

STRAIN CJB110

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAAATTATAGC
 GAGCATAAAGCAGCATCTCTCGACTTAAAGAAAGGAATTTCTAAACATTT
 ATATAAATAACAGCAGCTCTATTTTGAATCTTATACAGGAAGCATAACTA
 GTGACCCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATTTTAA
 TTTGCTTTTACCGCTTTTGAAGAGGCTCTTGTCTTCTCAGGTGTTAATTT
 AAAAGCTTATCATAAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAA
 AGAGTGTGGTCAAAATGCCCTTGTATCAATTTGAAGAAGGAGAGCGTCAA
 GTAGATGCTAGTTTATTAGAAAAGCATCTGTTTACCATATTGCTGATGA
 ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCG
 CCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAA
 GATGGCGATTGTGATTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGA
 TATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTATAACAGAAATGG
 CATGTACAGCCCTATTCTCTGAAAAGGAATCAATTTGGGTGAGGGCGCT
 GGTTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAATAAT
 TATCGGTGGTCTTATTAATCTCAGATGGTTATCATATAACAGCACCTAAGC
 CAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCA
 GGTATTGACTACAGTGAGATTGACTATATTAATGGTCACGGTACAGGTAC
 TCAAGCTAATGATAAAATGGAATAAATATGTATGGTAAGTTTTCCCGA
 CAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTACATACTCTAGGG
 GCTGCAGGTATTATCGAATTGATTAAATGTTTGTAGCGCAATAGAGGAACA
 GACTGTACAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCAGAAA
 ATTTTGTCTATCATCAAAAGAGAGAATACCAATAAGAAATGCTTTAAAT
 TTTTCGTTTGTCTTTTGGTGGAAATAATAGTGGTATCTTATTGTCTCTTT
 AGATTCACTCTAGAAAACATTACCTGCTAGAGAAAATCTTAAATGGCTA
 TCTTATCATCTGTTGCTTCCATTCTAAGAATGAATCACTTCTATAACC
 TATGAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
 AGGGGCTAGACCACCCAAAACCTGTCAACCCAGCACAAATTTAGGAAAATGG
 ATGATTTTCCAAAATGGTTGCCGTAACCAACAGCTCAAGCACTAATAGAA
 AGCAATATTAATCTAAAAAACAAGATACTTCAAAGTAGGAATGTATT
 TACAACACTTTCTGGACCGTTGAGGTTGTGAAGGTATTGAAAAGCAAA
 TCACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCTCGTTTACA
 GTAATGAATGCAGCAGCTGGTATGCTTCTATCATTTTAAATAACAGG
 TCCCTTATCTGTCACTTCGACAAATAGTGGAGCGCTTGATGGTATACAAT
 ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTGTGT
 TCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTAA
 CTATGATAGTCAAATGTTTGTGCGTTCTGATTATTGTTTCAACAGTCC
 TCTCTCGTCAAGCATTGGGATAATCTCCTATAATATTAGGTAGTAAACAA
 TTAATAATATAGCCATAAAACATTCAAGATGTGATGACTATTTTGTATGC
 TGGCCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAGATATCA
 AAGGTTTCGTTTGGAAATGAGCGGAAGAAGGCAGTTAGTTTCAAGTTATGAT
 TTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGTCTCTGG
 TCAGTTTGGATTTCATCTAATGGTGTGGTGAAGAACTGGACTATACTG
 TTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTCTATCTATTTCGATC
 TTTGGTGGTATCTCTTTTGTCTATTATTGAAAAAAGG

Table 75: Comparative Sequences relating to SAG0671

SEQ ID NO. 7510

STRAIN 1169NT

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAG
 CGAGCATAAACAGCATCTCTTCGACTTAAAGAAAGGAATTTCTAAACATT
 TATATAAAAATCAGGACTCTATTTTGAATCTTATACAGGAAGCATAACT
 AGTGACCCAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAATTTTAA
 ATTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATT
 TAAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGA
 AAGAGTGTGGTCAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCA
 AGTAGATGCTAGTTTATAGAAAAAGCATCTGTTTACCATATTGCTGATG
 AATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACC
 GCCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCA
 AGATGGCGATTGTGATTAGCTATTGTGGTGGCTGTGATGAGTTAAGTG
 ATATTTCTTTAGCAGGCTTACATCACTAGGAGCTATTAATACAGAAATG
 GCATGTGAGCCCTATTCTTCTGGAAGAAAGGAATCAATTTGGGTGAGGCGC
 TGGTTTGTGTGTTCTTGTCAAAGATCAGTCCCTAGCTAAATATGGAAGAAA
 TTATCGGTGGTCTTATTACTTTCAGATGGTTATCATATAACAGCACCTAAG
 CCAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGC
 AGGTATTGACTACAGTGAGATTGACTATATTACGGTCAACGGTACAGGTA
 CTCAAGCTAATGATAAAATGGAAGAAATATGTTAGTAAAGTTTTCCTCG
 ACAACGACATTGATCAGCAGTACCAAGGGGCAACCGGTCATACCTTAGG
 GGCTGCAGGTATTATCGAATTGATTAAATTGTTTAGCGCAATAGAGGAAC
 AGACTGTACCAGCACTAAAAATGAGATTGGGATAGAAGGTTTCCAGAA
 AATTTTGTCTATCATCAAAGAGAGAATACCCATAAGAAATGCTTTAA
 TTTTTCGTTTGTCTTTGGTGGAAATAATAGTGGTATCTTATTGTCTATCT
 TAGATTCACTCTAGAAACATTACCTGCTAGAGAAATCTTAAATGGCT
 ATCTTATCATCTGTTGCTTCCATTCTAAGAATGAATCACTTTCTATAAC
 CTATGAAAAGTTGTAGTAAATTTCAACGACTTTGAAGCAATTACGCTTTA
 AAGGGGCTAGACCACCCAAACTGTCAACCCAGCACAAATTTAGGAAATG
 GATGATTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGA
 AAGCAATATTAATCTAAAAACAAGATACTTCAAAGTAGGAATTGTAT
 TTACAACACTTTCTGGACCAAGTTGAGGTTGTTGAAGGTATTGAAAAGCAA
 ATCACAACAGAAGGATATGCACATGTTCTGCTTCACGATTCCCGTTTAC
 AGTAATGAATGCAGCAGCTGGTATGCTTCTATCATTTTAAATAACAG
 GTCCTTTATCTGTCAATTCGACAAATAGTGGAGCGCTTGATGGTATACAA
 TATGCCAAGGAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGT
 TTCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTA
 ACTATGATAGTCAAATGTTTGTGGTTCTGATTATTGTTTCAACAGTCT
 CTCTCTCGTCAAGCATGGATAATTCTCTATAATATTAGGTAGTAAACA
 ATTTAAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGTATG
 CTGCGCTTCAAATTTTATTATCAGACTTAGGACTAACCATAAAGATATC
 AAAGGTTTCTGTTGGAAATGAGCGGAAGAAGGCAGTTAGTTTCAAGATTATGA
 TTTCTTAGCGAATCTGTCTGAGTATTATAATATGCCAACCTTGCTCTG
 GTCAGTTTGGATTTCATCTAATGGTGGCTGGTGAAGAACTGGACTATACT
 GTTAATGAAGTATAGAAAAGGGCTATTATTAGTCTTATCTTATTCGAT
 CTTTGGTGGTATCTCTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7511

STRAIN JM9130013

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGCGAG
 CATAAACAGCATCTCTTCGACTTAAAGAAAGGAATTTCTAAACATTATATA
 TAAAAATCAGGACTCTATTTTGAATCTTATACAGGAAGCATAACTAGTG
 ACCGAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAATTTTAAATTT
 GCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTTAAA
 AGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGAAAGA
 GTGCTGGTCAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCAAGTA
 GATGCTAGTTTATAGAAAAAGCATCTGTTTACCATATTGCTGATGAATT
 GATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCGCTT
 GTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAAGAT
 GGCAGATTGTGATTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGATAT
 TTCTTTAGCAGGCTTACATCACTAGGAGCTATTAATACAGAAATGGCAT
 GTCAGCCCTATTCTTCTGGAAGAAAGGAATCAATTTGGGTGAGGCGCTGGT
 TTTGTTGTTCTTGTCAAAGATCAGTCCCTAGCTAAATATGGAAGAAATAT
 CGGTGGTCTTATTACTTTCAGATGGTTATCATATAACAGCACCTAAGCCAA
 CAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCAGGT
 ATTGACTACAGTGAGATTGACTATATTACGGTCAACGGTACAGGTACTCA
 AGCTAATGATAAAATGGAAGAAATATGTTAGTAAAGTTTTCCTCGACAA
 CGACATTGATCAGCAGTACCAAGGGGCAACCGGTCATACTCTAGGGGCT
 GCAGGTATTATCGAATTGATTAAATTGTTTAGCGGCAATAGAGGAACAGAC
 TGTACAGCACTAAAAATGAGATTGGGATAGAAGGTTTTCAGAAAATTT
 TTGCTATCATCAAAGAGAGAATAACCAATAAGAAATGCTTTAAATTTT
 TCGTTTGTCTTTGGTGGAAATAATAGTGGTGTCTTATTGTCTCTTTAGA
 TTCACCTCTAGAAACATTACCTGCTAGAGAAATCTTAAATGGCTATCT
 TATCATCTGTTGCTTCCATTTCTAAGAAATGAATCACTTTCTATAACCTAT
 GAAAAAGTTGCTAGTAAATTTCAACGACTTTGAAGCAATTACGCTTTAAGG
 GGCTAGACCCCAAACTGTCAACCCAGCACAAATTTAGGAAATGGATG
 ATTTTTCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAAAGC
 AATATTAAATCTAAAAACAAGATACTTCAAAGTAGGAATTGTATTAC
 AACACTTTCTGGACCAAGTTGAGGTTGTTGAAGGTATTGAAAAGCAATCA
 CAACAGAGGATATGCACATGTTCTGCTTCAAGATTCCCGTTTACAGTA
 ATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTAAATAACAGGTCC
 TTTATCTGTCATTTTCGACAAATAGTGGAGCGCTTGATGGTATACAAATATG

Table 75: Comparative Sequences relating to SAG0671

CCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGTTCCT
 GCTAATCAGTGGACAGACATGAGTTTATGTTGGTGGCAACAATTAACCTA
 TGATAGTCAAATCTTTGTCGGTTCGATTATTGTTACGACACAGTCCTCT
 CTCGTCAAGCATGGATAAATCTCCTATAATATTAGGTAGTAAACAATTA
 AAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGTGCTGC
 GCTTCAAATTTTATATCAGACTTAGGACTAACCATAAAGATATCAAG
 GTTTCGTTTGAATGAGCGGAAGAGGCAGTTAGTTTCAAGATTATGATTTC
 TTAGCGAAGCTGTCTGAGTATTATAATATGCCAAACCTTGTCTCTGGTCA
 GTTTGGATTTCATCTAATGGTGTCTGGTGAAGAACTGGACTATACGTGA
 ATGAAAGTATAGAAAAGGGCTATTATTAGTCCTATCTTATTCGATCTTC
 GGTGATCTCTTTTGTCTATTATTGAAAAAGG

PRETTY of: /biotmp/msal18688.2{*} April 9, 2003 02:55 ..

	1				50
msal18688.2{361_18RS21}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msal18688.2{361_A909}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msal18688.2{361_COH1}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msal18688.2{361_H36B}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msal18688.2{361_JM9130013}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msal18688.2{361_M732}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msal18688.2{GBS361_2603}	atgagcgtat	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msal18688.2{361_090}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msal18688.2{361_1169NT}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msal18688.2{361_CJB110}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msal18688.2{361_M781}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
Consensus	*****	*****	*****	*****	*****
	51				100
msal18688.2{361_18RS21}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAAGAA	GGAATTTCTA
msal18688.2{361_A909}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAAGAA	GGAATTTCTA
msal18688.2{361_COH1}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAAGAA	GGAATTTCTA
msal18688.2{361_H36B}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAAGAA	GGAATTTCTA
msal18688.2{361_JM9130013}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAAGAA	GGAATTTCTA
msal18688.2{361_M732}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAAGAA	GGAATTTCTA
msal18688.2{GBS361_2603}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAAGAA	GGAATTTCTA
msal18688.2{361_090}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAAGAA	GGAATTTCTA
msal18688.2{361_1169NT}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAAGAA	GGAATTTCTA
msal18688.2{361_CJB110}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAAGAA	GGAATTTCTA
msal18688.2{361_M781}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAAGAA	GGAATTTCTA
Consensus	*****	*****	*****	*****	*****
	101				150
msal18688.2{361_18RS21}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msal18688.2{361_A909}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msal18688.2{361_COH1}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msal18688.2{361_H36B}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msal18688.2{361_JM9130013}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msal18688.2{361_M732}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msal18688.2{GBS361_2603}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msal18688.2{361_090}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msal18688.2{361_1169NT}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msal18688.2{361_CJB110}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msal18688.2{361_M781}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
Consensus	*****	*****	*****	*****	*****
	151				200
msal18688.2{361_18RS21}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msal18688.2{361_A909}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msal18688.2{361_COH1}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msal18688.2{361_H36B}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msal18688.2{361_JM9130013}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msal18688.2{361_M732}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msal18688.2{GBS361_2603}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msal18688.2{361_090}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msal18688.2{361_1169NT}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msal18688.2{361_CJB110}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msal18688.2{361_M781}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
Consensus	*****	*****	*****	*****	*****
	201				250
msal18688.2{361_18RS21}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msal18688.2{361_A909}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msal18688.2{361_COH1}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msal18688.2{361_H36B}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msal18688.2{361_JM9130013}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msal18688.2{361_M732}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msal18688.2{GBS361_2603}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msal18688.2{361_090}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msal18688.2{361_1169NT}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msal18688.2{361_CJB110}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msal18688.2{361_M781}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
Consensus	*****	*****	*****	*****	*****

Table 75: Comparative Sequences relating to SAG0671

	251		300
msa118688.2{361_18RS21}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_A909}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_COH1}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_H36B}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_JM9130013}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_M732}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{GBS361_2603}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_090}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_1169NT}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_CJB110}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_M781}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
Consensus	*****	*****	*****
msa118688.2{361_18RS21}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_A909}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_COH1}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_H36B}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_JM9130013}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_M732}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{GBS361_2603}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_090}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_1169NT}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_CJB110}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_M781}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
Consensus	*****	*****	*****
msa118688.2{361_18RS21}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_A909}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_COH1}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_H36B}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_JM9130013}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_M732}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{GBS361_2603}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_090}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_1169NT}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_CJB110}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_M781}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
Consensus	*****	*****	*****
msa118688.2{361_18RS21}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_A909}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_COH1}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_H36B}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_JM9130013}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_M732}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{GBS361_2603}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_090}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_1169NT}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_CJB110}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_M781}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
Consensus	*****	*****	*****
msa118688.2{361_18RS21}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_A909}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_COH1}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_H36B}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_JM9130013}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_M732}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{GBS361_2603}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_090}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_1169NT}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_CJB110}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_M781}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
Consensus	*****	*****	*****
msa118688.2{361_18RS21}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_A909}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_COH1}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_H36B}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_JM9130013}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_M732}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{GBS361_2603}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_090}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_1169NT}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_CJB110}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_M781}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
Consensus	*****	*****	*****

Table 75: Comparative Sequences relating to SAG0671

Consensus	*****	*****	*****	*****	*****
	551				600
msa118688.2{361_18RS21}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_A909}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_COH1}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_H36B}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_JM9130013}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_M732}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{GBS361_2603}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_090}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_1169NT}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_CJB110}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_M781}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
Consensus	*****	*****	*****	*****	*****
	601				650
msa118688.2{361_18RS21}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_A909}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_COH1}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_H36B}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_JM9130013}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_M732}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{GBS361_2603}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_090}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_1169NT}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_CJB110}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_M781}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
Consensus	*****	*****	*****	*****	*****
	651				700
msa118688.2{361_18RS21}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_A909}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_COH1}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_H36B}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_JM9130013}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_M732}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{GBS361_2603}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_090}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_1169NT}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_CJB110}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_M781}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
Consensus	*****	*****	*****	*****	*****
	701				750
msa118688.2{361_18RS21}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_A909}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_COH1}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_H36B}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_JM9130013}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_M732}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{GBS361_2603}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_090}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_1169NT}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_CJB110}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_M781}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
Consensus	*****	*****	*****	*****	*****
	751				800
msa118688.2{361_18RS21}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_A909}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_COH1}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_H36B}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_JM9130013}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_M732}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{GBS361_2603}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_090}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_1169NT}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_CJB110}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_M781}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
Consensus	*****	*****	*****	*****	*****
	801				850
msa118688.2{361_18RS21}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_A909}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_COH1}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_H36B}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_JM9130013}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_M732}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{GBS361_2603}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_090}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_1169NT}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_CJB110}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{361_M781}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAT	GGTCACGGTA
Consensus	*****	*****	*****	*****	*****
	851				900
msa118688.2{361_18RS21}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_A909}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_COH1}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_H36B}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_JM9130013}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_M732}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{GBS361_2603}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_090}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_1169NT}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_CJB110}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_M781}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
Consensus	*****	*****	*****	*****	*****
	901				950
msa118688.2{361_18RS21}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_A909}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_COH1}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_H36B}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_JM9130013}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_M732}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{GBS361_2603}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_090}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_1169NT}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_CJB110}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_M781}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
Consensus	*****	*****	*****	*****	*****
	951				1000
msa118688.2{361_18RS21}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_A909}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_COH1}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_H36B}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_JM9130013}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_M732}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{GBS361_2603}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_090}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_1169NT}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_CJB110}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_M781}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
Consensus	*****	*****	*****	*****	*****
	1001				1050
msa118688.2{361_18RS21}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_A909}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_COH1}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_H36B}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_JM9130013}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_M732}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{GBS361_2603}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_090}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_1169NT}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_CJB110}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_M781}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
Consensus	*****	*****	*****	*****	*****
	1051				1100
msa118688.2{361_18RS21}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_A909}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_COH1}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_H36B}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_JM9130013}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_M732}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{GBS361_2603}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_090}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_1169NT}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_CJB110}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_M781}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
Consensus	*****	*****	*****	*****	*****
	1101				1150
msa118688.2{361_18RS21}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTGT
msa118688.2{361_A909}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTGT
msa118688.2{361_COH1}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTGT
msa118688.2{361_H36B}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTGT
msa118688.2{361_JM9130013}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTGT
msa118688.2{361_M732}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTGT
msa118688.2{GBS361_2603}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTGT
msa118688.2{361_090}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTGT
msa118688.2{361_1169NT}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTGT
msa118688.2{361_M781}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTGT
Consensus	*****	*****	*****	*****	*****

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{361_CJB110}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	aTCTTATTGT		
msa118688.2{361_M781}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	aTCTTATTGT		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1151	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA	1200
msa118688.2{361_A909}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{361_COH1}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{361_H36B}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{361_JM9130013}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{361_M732}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{GBS361_2603}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{361_090}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{361_1169NT}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{361_CJB110}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{361_M781}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1201	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC	1250
msa118688.2{361_A909}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{361_COH1}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{361_H36B}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{361_JM9130013}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{361_M732}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{GBS361_2603}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{361_090}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{361_1169NT}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{361_CJB110}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{361_M781}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1251	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC	1300
msa118688.2{361_A909}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{361_COH1}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{361_H36B}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{361_JM9130013}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{361_M732}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{GBS361_2603}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{361_090}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{361_1169NT}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{361_CJB110}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{361_M781}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1301	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG	1350
msa118688.2{361_A909}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{361_COH1}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{361_H36B}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{361_JM9130013}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{361_M732}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{GBS361_2603}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{361_090}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{361_1169NT}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{361_CJB110}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{361_M781}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1351	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT	1400
msa118688.2{361_A909}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{361_COH1}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{361_H36B}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{361_JM9130013}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{361_M732}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{GBS361_2603}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{361_090}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{361_1169NT}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{361_CJB110}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{361_M781}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1401	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA	1450
msa118688.2{361_A909}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA		
msa118688.2{361_COH1}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA		
msa118688.2{361_H36B}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA		
msa118688.2{361_JM9130013}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA		
msa118688.2{361_M732}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA		
msa118688.2{GBS361_2603}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA		
msa118688.2{361_090}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA		

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{361_1169NT}	AATAGAAAGC	AATATTAATC	TAAAAAAACA	AGATACTTCA	AAAGTAGGAA		
msa118688.2{361_CJB110}	AATAGAAAGC	AATATTAATC	TAAAAAAACA	AGATACTTCA	AAAGTAGGAA		
msa118688.2{361_M781}	AATAGAAAGC	AATATTAATC	TAAAAAAACA	AGATACTTCA	AAAGTAGGAA		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1451	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA	1500
msa118688.2{361_A909}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA		
msa118688.2{361_COH1}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA		
msa118688.2{361_H36B}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA		
msa118688.2{361_JM9130013}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA		
msa118688.2{361_M732}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA		
msa118688.2{GBS361_2603}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA		
msa118688.2{361_090}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA		
msa118688.2{361_1169NT}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA		
msa118688.2{361_CJB110}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA		
msa118688.2{361_M781}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1501	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC	1550
msa118688.2{361_A909}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC		
msa118688.2{361_COH1}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC		
msa118688.2{361_H36B}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC		
msa118688.2{361_JM9130013}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC		
msa118688.2{361_M732}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC		
msa118688.2{GBS361_2603}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC		
msa118688.2{361_090}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC		
msa118688.2{361_1169NT}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC		
msa118688.2{361_CJB110}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC		
msa118688.2{361_M781}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1551	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA	1600
msa118688.2{361_A909}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA		
msa118688.2{361_COH1}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA		
msa118688.2{361_H36B}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA		
msa118688.2{361_JM9130013}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA		
msa118688.2{361_M732}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA		
msa118688.2{GBS361_2603}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA		
msa118688.2{361_090}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA		
msa118688.2{361_1169NT}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA		
msa118688.2{361_CJB110}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA		
msa118688.2{361_M781}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1601	TAACAGGTCC	TTTATCTGTC	ATTTCGACAA	ATAGTGGAGC	GCTTGATGGT	1650
msa118688.2{361_A909}	TAACAGGTCC	TTTATCTGTC	ATTTCGACAA	ATAGTGGAGC	GCTTGATGGT		
msa118688.2{361_COH1}	TAACAGGTCC	TTTATCTGTC	ATTTCGACAA	ATAGTGGAGC	GCTTGATGGT		
msa118688.2{361_H36B}	TAACAGGTCC	TTTATCTGTC	ATTTCGACAA	ATAGTGGAGC	GCTTGATGGT		
msa118688.2{361_JM9130013}	TAACAGGTCC	TTTATCTGTC	ATTTCGACAA	ATAGTGGAGC	GCTTGATGGT		
msa118688.2{361_M732}	TAACAGGTCC	TTTATCTGTC	ATTTCGACAA	ATAGTGGAGC	GCTTGATGGT		
msa118688.2{GBS361_2603}	TAACAGGTCC	TTTATCTGTC	ATTTCGACAA	ATAGTGGAGC	GCTTGATGGT		
msa118688.2{361_090}	TAACAGGTCC	TTTATCTGTC	ATTTCGACAA	ATAGTGGAGC	GCTTGATGGT		
msa118688.2{361_1169NT}	TAACAGGTCC	TTTATCTGTC	ATTTCGACAA	ATAGTGGAGC	GCTTGATGGT		
msa118688.2{361_CJB110}	TAACAGGTCC	TTTATCTGTC	ATTTCGACAA	ATAGTGGAGC	GCTTGATGGT		
msa118688.2{361_M781}	TAACAGGTCC	TTTATCTGTC	ATTTCGACAA	ATAGTGGAGC	GCTTGATGGT		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1651	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT	1700
msa118688.2{361_A909}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT		
msa118688.2{361_COH1}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT		
msa118688.2{361_H36B}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT		
msa118688.2{361_JM9130013}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT		
msa118688.2{361_M732}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT		
msa118688.2{GBS361_2603}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT		
msa118688.2{361_090}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT		
msa118688.2{361_1169NT}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT		
msa118688.2{361_CJB110}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT		
msa118688.2{361_M781}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1701	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC	1750
msa118688.2{361_A909}	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC		
msa118688.2{361_COH1}	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC		
msa118688.2{361_H36B}	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC		
msa118688.2{361_JM9130013}	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC		
msa118688.2{361_M732}	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC		
msa118688.2{GBS361_2603}	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC		

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{361_090}	TCTTGTTCCT	GCTAATCAGT	GGACAGACAT	GAGTTTATG	TGGTGGCAAC	
msa118688.2{361_1169NT}	TCTTGTTCCT	GCTAATCAGT	GGACAGACAT	GAGTTTATG	TGGTGGCAAC	
msa118688.2{361_CJB110}	TCTTGTTCCT	GCTAATCAGT	GGACAGACAT	GAGTTTATG	TGGTGGCAAC	
msa118688.2{361_M781}	TCTTGTTCCT	GCTAATCAGT	GGACAGACAT	GAGTTTATG	TGGTGGCAAC	
Consensus	*****	*****	*****	*****	*****	
msa118688.2{361_18RS21}	1751	AATTAACTA	TGATAGTCAA	ATGTTTGTCTG	GTTCTGATTA	1800
msa118688.2{361_A909}	AATTAACTA	TGATAGTCAA	ATGTTTGTCTG	GTTCTGATTA	TTGTTTCAGCA	
msa118688.2{361_COH1}	AATTAACTA	TGATAGTCAA	ATGTTTGTCTG	GTTCTGATTA	TTGTTTCAGCA	
msa118688.2{361_H36B}	AATTAACTA	TGATAGTCAA	ATGTTTGTCTG	GTTCTGATTA	TTGTTTCAGCA	
msa118688.2{361_JM9130013}	AATTAACTA	TGATAGTCAA	ATGTTTGTCTG	GTTCTGATTA	TTGTTTCAGCA	
msa118688.2{361_M732}	AATTAACTA	TGATAGTCAA	ATGTTTGTCTG	GTTCTGATTA	TTGTTTCAGCA	
msa118688.2{GBS361_2603}	AATTAACTA	TGATAGTCAA	ATGTTTGTCTG	GTTCTGATTA	TTGTTTCAGCA	
msa118688.2{361_090}	AATTAACTA	TGATAGTCAA	ATGTTTGTCTG	GTTCTGATTA	TTGTTTCAGCA	
msa118688.2{361_1169NT}	AATTAACTA	TGATAGTCAA	ATGTTTGTCTG	GTTCTGATTA	TTGTTTCAGCA	
msa118688.2{361_CJB110}	AATTAACTA	TGATAGTCAA	ATGTTTGTCTG	GTTCTGATTA	TTGTTTCAGCA	
msa118688.2{361_M781}	AATTAACTA	TGATAGTCAA	ATGTTTGTCTG	GTTCTGATTA	TTGTTTCAGCA	
Consensus	*****	*****	*****	*****	*****	
msa118688.2{361_18RS21}	1801	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	1850
msa118688.2{361_A909}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG	
msa118688.2{361_COH1}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG	
msa118688.2{361_H36B}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG	
msa118688.2{361_JM9130013}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG	
msa118688.2{361_M732}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG	
msa118688.2{GBS361_2603}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG	
msa118688.2{361_090}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG	
msa118688.2{361_1169NT}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG	
msa118688.2{361_CJB110}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG	
msa118688.2{361_M781}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG	
Consensus	*****	*****	*****	*****	*****	
msa118688.2{361_18RS21}	1851	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	1900
msa118688.2{361_A909}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT	
msa118688.2{361_COH1}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT	
msa118688.2{361_H36B}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT	
msa118688.2{361_JM9130013}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT	
msa118688.2{361_M732}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT	
msa118688.2{GBS361_2603}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT	
msa118688.2{361_090}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT	
msa118688.2{361_1169NT}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT	
msa118688.2{361_CJB110}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT	
msa118688.2{361_M781}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT	
Consensus	*****	*****	*****	*****	*****	
msa118688.2{361_18RS21}	1901	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	1950
msa118688.2{361_A909}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA	
msa118688.2{361_COH1}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA	
msa118688.2{361_H36B}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA	
msa118688.2{361_JM9130013}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA	
msa118688.2{361_M732}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA	
msa118688.2{GBS361_2603}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA	
msa118688.2{361_090}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA	
msa118688.2{361_1169NT}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA	
msa118688.2{361_CJB110}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA	
msa118688.2{361_M781}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA	
Consensus	*****	*****	*****	*****	*****	
msa118688.2{361_18RS21}	1951	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	2000
msa118688.2{361_A909}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTTCAGA	
msa118688.2{361_COH1}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTTCAGA	
msa118688.2{361_H36B}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTTCAGA	
msa118688.2{361_JM9130013}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTTCAGA	
msa118688.2{361_M732}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTTCAGA	
msa118688.2{GBS361_2603}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTTCAGA	
msa118688.2{361_090}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTTCAGA	
msa118688.2{361_1169NT}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTTCAGA	
msa118688.2{361_CJB110}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTTCAGA	
msa118688.2{361_M781}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTTCAGA	
Consensus	*****	*****	*****	*****	*****	
msa118688.2{361_18RS21}	2001	TTATGATTTT	TTAGCGAAGT	TGTCTGAGTA	TTATAATATG	2050
msa118688.2{361_A909}	TTATGATTTT	TTAGCGAAGT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG	
msa118688.2{361_COH1}	TTATGATTTT	TTAGCGAAGT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG	
msa118688.2{361_H36B}	TTATGATTTT	TTAGCGAAGT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG	
msa118688.2{361_JM9130013}	TTATGATTTT	TTAGCGAAGT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG	
msa118688.2{361_M732}	TTATGATTTT	TTAGCGAAGT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG	

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{GBS361_2603}	TTATGATTTC	TTAGCGAACT	TGCTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_090}	TTATGATTTC	TTAGCGAACT	TGCTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_1169NT}	TTATGATTTC	TTAGCGAACT	TGCTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_CJB110}	TTATGATTTC	TTAGCGAACT	TGCTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_M781}	TTATGATTTC	TTAGCGAACT	TGCTCTGAGTA	TTATAATATG	CCAAACCTTG
Consensus	*****	*****	*****	*****	*****
2051					
msa118688.2{361_18RS21}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_A909}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_COH1}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_H36B}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_JM9130013}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_M732}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{GBS361_2603}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_090}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_1169NT}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_CJB110}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_M781}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
Consensus	*****	*****	*****	*****	*****
2101					
msa118688.2{361_18RS21}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_A909}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_COH1}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_H36B}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_JM9130013}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_M732}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{GBS361_2603}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_090}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_1169NT}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_CJB110}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_M781}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
Consensus	*****	*****	*****	*****	*****
2151					
msa118688.2{361_18RS21}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_A909}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_COH1}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_H36B}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_JM9130013}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_M732}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{GBS361_2603}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_090}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_1169NT}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_CJB110}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_M781}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
Consensus	*****	*****	*****	*****	***

SEQ ID NO. 7512

STRAIN 2603 frame: 1

MSVYVSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESITSGSITSDPEVPEQ
 YKDETRNFKAFAFEALASSGVNLKAYHNIIVCLGTSLGKKSAGQNALYQFEEGERQV
 DASLLEKASVYHIADELMAYHDIIVGASYVISTACASNNNAVILGTQLLDQDCLDAICGG
 CDELSDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYKGIIGGL
 ITSDGYHITAPKPTGEGAAQIAKQLVTOAGIDYSEIDYINGHGTGTQANDKMEKNMYGKF
 FPTTLISSTKGQTGHTLGAAGIIELINCLAAIEEQTPATKNEIGIEGFENFVYHOKR
 EYPRNALNFSFAFGGNNSGVLLSSLDSPLETLARENLMKMAILSSVASISKNESLSITY
 EKVASNFDFEALRFKGRPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTS
 KVGIVFTTSLGPPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSV
 ISTNSGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWQQLNYSQMFVGSIDYCSA
 QVLSRQALDNPILGSKQLKYSKHTFTDVTMIFDAALQNLSDGLTIKDIKGFVWNER
 KKAUSSDYDFLANLSEYNNMPLNASGQFGFSSNGAGEELDYTVNESIEKGYLVLSYSIF
 GGISFAIIEKR

SEQ ID NO. 7513

STRAIN 090 frame: 3

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESITSGSITSDPEVPEQYKDE
 TRNFKAFAFEALASSGVNLKAYHNIIVCLGTSLGKKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDIIVGASYVISTACASNNNAVILGTQLLDQDCLDAICGG
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYKGIIGGLITSD
 GYHITAPKPTGEGAAQIAKQLVTOAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFPTT
 TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTPATKNEIGIEGFENFVYHOKREYPI
 RNALNFSFAFGGNNSGVLLSSLDSPLETLARENLMKMAILSSVASISKNESLSITYEYKVA
 SNFDFEALRFKGRPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVG
 VFTTSLGPPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWQQLNYSQMFVGSIDYCSAQVLS
 RQALDNPILGSKQLKYSKHTFTDVTMIFDAALQNLSDGLTIKDIKGFVWNERKKA
 USSDYDFLANLSEYNNMPLNASGQFGFSSNGAGEELDYTVNESIEKGYLVLSYSIFGGIS
 FAIIEKR

SEQ ID NO. 7514

STRAIN A909 frame: 3

Table 75: Comparative Sequences relating to SAG0671

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLYKAYHNI AVCLGTS LGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDI VGASYVISTACASASNNAVILGTQLLDGDCDLAICGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYKGIIGGLITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSSTKGQTGHTLGAAGII ELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
 RNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKRGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
 RQALDNSPI ILGSKQLKYSHKTFDVTI FDAALQNLSDLG LTI KD IKGFVWNERKKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYIFGGIS
 FAIEKR

SEQ ID NO. 7515

STRAIN H36B frame: 3

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLYKAYHNI AVCLGTS LGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDI VGASYVISTACASASNNAVILGTQLLDGDCDLAICGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYKGIIGGLITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSSTKGQTGHTLGAAGII ELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
 RNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKRGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
 RQALDNSPI ILGSKQLKYSHKTFDVTI FDAALQNLSDLG LTI KD IKGFVWNERKKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYIFGGIS
 FAIEKR

SEQ ID NO. 7516

STRAIN 18RS21 frame: 3

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLYKAYHNI AVCLGTS LGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDI VGASYVISTACASASNNAVILGTQLLDGDCDLAICGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYKGIIGGLITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSSTKGQTGHTLGAAGII ELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
 RNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKRGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
 RQALDNSPI ILGSKQLKYSHKTFDVTI FDAALQNLSDLG LTI KD IKGFVWNERKKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYIFGGIS
 FAIEKR

SEQ ID NO. 7517

STRAIN M732 frame: 3

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLYKAYHNI AVCLGTS LGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDI VGASYVISTACASASNNAVILGTQLLDGDCDLAICGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYKGIIGGLITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSSTKGQTGHTLGAAGII ELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
 RNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKRGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
 RQALDNSPI ILGSKQLKYSHKTFDVTI FDAALQNLSDLG LTI KD IKGFVWNERKKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYIFGGIS
 FAIEKR

SEQ ID NO. 7518

STRAIN COH1 frame: 3

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLYKAYHNI AVCLGTS LGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDI VGASYVISTACASASNNAVILGTQLLDGDCDLAICGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYKGIIGGLITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSSTKGQTGHTLGAAGII ELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
 RNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKRGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
 RQALDNSPI ILGSKQLKYSHKTFDVTI FDAALQNLSDLG LTI KD IKGFVWNERKKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYIFGGIS
 FAIEKR

SEQ ID NO. 7519

STRAIN M781 frame: 3

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLYKAYHNI AVCLGTS LGGKSAGQNALYQFEEGERQVDASL

Table 75: Comparative Sequences relating to SAG0671

LEKASVYHIADELMAYHDI VGASYVISTACASANNVILGTQLLDGDCDLAICGGCDEL
SDISLAGFTSLGAINTMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTOAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQVTPATKNEIGIEGFPENFVYHOKREYPI
RNALNFSFAFGGNNNGI LLSLSDSPLTLTPARENLMKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKARGPPKTVNPAQFRKMDDFSKMVAVTTAQAALIESNINLKKQDTSKVGI
VFTTSLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGSYCSAQVLS
RQALDNPPIILGSKQLKYSKHTFTDVMITFDAALQNLSDGLTIDKIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYVLVLSYSIFGGIS
FAIIEKR

SEQ ID NO. 7520

STRAIN CJB110 frame: 3

VSGIGIISLGNKYNSEHKQHLFDLKEGISKHLYKNHDSILESITSGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIACVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDI VGASYVISTACASANNVILGTQLLDGDCDLAICGGCDEL
SDISLAGFTSLGAINTMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTOAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQVTPATKNEIGIEGFPENFVYHOKREYPI
RNALNFSFAFGGNNNGI LLSLSDSPLTLTPARENLMKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKARGPPKTVNPAQFRKMDDFSKMVAVTTAQAALIESNINLKKQDTSKVGI
VFTTSLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGSYCSAQVLS
RQALDNPPIILGSKQLKYSKHTFTDVMITFDAALQNLSDGLTIDKIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYVLVLSYSIFGGIS
FAIIEKR

SEQ ID NO. 7521

STRAIN 1169NT frame: 3

VSGIGIISLGNKYNSEHKQHLFDLKEGISKHLYKNHDSILESITSGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIACVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDI VGASYVISTACASANNVILGTQLLDGDCDLAICGGCDEL
SDISLAGFTSLGAINTMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTOAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQVTPATKNEIGIEGFPENFVYHOKREYPI
RNALNFSFAFGGNNNGI LLSLSDSPLTLTPARENLMKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKARGPPKTVNPAQFRKMDDFSKMVAVTTAQAALIESNINLKKQDTSKVGI
VFTTSLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGSYCSAQVLS
RQALDNPPIILGSKQLKYSKHTFTDVMITFDAALQNLSDGLTIDKIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYVLVLSYSIFGGIS
FAIIEKR

SEQ ID NO. 7522

STRAIN JM9130013 frame: 3

VSGIGIISLGNKYNSEHKQHLFDLKEGISKHLYKNHDSILESITSGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIACVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDI VGASYVISTACASANNVILGTQLLDGDCDLAICGGCDEL
SDISLAGFTSLGAINTMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTOAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQVTPATKNEIGIEGFPENFVYHOKREYPI
RNALNFSFAFGGNNNGI LLSLSDSPLTLTPARENLMKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKARGPPKTVNPAQFRKMDDFSKMVAVTTAQAALIESNINLKKQDTSKVGI
VFTTSLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGSYCSAQVLS
RQALDNPPIILGSKQLKYSKHTFTDVMITFDAALQNLSDGLTIDKIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYVLVLSYSIFGGIS
FAIIEKR

PRETTY of: /biotmp/msa118713.2{*} April 9, 2003 02:54 ..

	1		50
msa118713.2{361_090}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE	GISKHLYKNH DSILESITGS
msa118713.2{361_1169NT}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE	GISKHLYKNH DSILESITGS
msa118713.2{361_CJB110}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE	GISKHLYKNH DSILESITGS
msa118713.2{361_M781}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE	GISKHLYKNH DSILESITGS
msa118713.2{361_18RS21}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE	GISKHLYKNH DSILESITGS
msa118713.2{361_A909}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE	GISKHLYKNH DSILESITGS
msa118713.2{361_COH1}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE	GISKHLYKNH DSILESITGS
msa118713.2{361_H36B}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE	GISKHLYKNH DSILESITGS
msa118713.2{361_JM9130013}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE	GISKHLYKNH DSILESITGS
msa118713.2{361_M732}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE	GISKHLYKNH DSILESITGS
msa118713.2{GBS361_2603}	msvyVSGIGI	ISSLGKNYSE HKQHLFDLKE	GISKHLYKNH DSILESITGS
Consensus	*****	*****	*****
	51		100
msa118713.2{361_090}	ITSDPEVPEQ	YKDETRNFKF AFTAFEEALA	SSGVNLKAYH NIAVCLGTSL
msa118713.2{361_1169NT}	ITSDPEVPEQ	YKDETRNFKF AFTAFEEALA	SSGVNLKAYH NIAVCLGTSL
msa118713.2{361_CJB110}	ITSDPEVPEQ	YKDETRNFKF AFTAFEEALA	SSGVNLKAYH NIAVCLGTSL
msa118713.2{361_M781}	ITSDPEVPEQ	YKDETRNFKF AFTAFEEALA	SSGVNLKAYH NIAVCLGTSL
msa118713.2{361_18RS21}	ITSDPEVPEQ	YKDETRNFKF AFTAFEEALA	SSGVNLKAYH NIAVCLGTSL

Table 75: Comparative Sequences relating to SAG0671

msa118713.2{361_A909}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
msa118713.2{361_COH1}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
msa118713.2{361_H36B}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
msa118713.2{361_JM9130013}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
msa118713.2{361_M732}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
msa118713.2{GBS361_2603}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_1169NT}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_CJB110}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_M781}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_18RS21}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_A909}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_COH1}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_H36B}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_JM9130013}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_M732}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{GBS361_2603}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_1169NT}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_CJB110}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_M781}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_18RS21}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_A909}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_COH1}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_H36B}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_JM9130013}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_M732}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{GBS361_2603}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_1169NT}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_CJB110}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_M781}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_18RS21}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_A909}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_COH1}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_H36B}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_JM9130013}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_M732}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{GBS361_2603}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_1169NT}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_CJB110}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_M781}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_18RS21}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_A909}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_COH1}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_H36B}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_JM9130013}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_M732}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{GBS361_2603}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	FPTTTLISST	KGQTGHTLGA	AGIIEINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_1169NT}	FPTTTLISST	KGQTGHTLGA	AGIIEINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_CJB110}	FPTTTLISST	KGQTGHTLGA	AGIIEINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_M781}	FPTTTLISST	KGQTGHTLGA	AGIIEINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_18RS21}	FPTTTLISST	KGQTGHTLGA	AGIIEINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_A909}	FPTTTLISST	KGQTGHTLGA	AGIIEINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_COH1}	FPTTTLISST	KGQTGHTLGA	AGIIEINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_H36B}	FPTTTLISST	KGQTGHTLGA	AGIIEINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_JM9130013}	FPTTTLISST	KGQTGHTLGA	AGIIEINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_M732}	FPTTTLISST	KGQTGHTLGA	AGIIEINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{GBS361_2603}	FPTTTLISST	KGQTGHTLGA	AGIIEINCL	AAIEBQTVPA	TKNEIGIEGF
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	PENFVYHQKR	EYPIRNALNF	SFAFGGNSG	ILLSSLDSP	ETLPARENLK
msa118713.2{361_1169NT}	PENFVYHQKR	EYPIRNALNF	SFAFGGNSG	ILLSSLDSP	ETLPARENLK
msa118713.2{361_CJB110}	PENFVYHQKR	EYPIRNALNF	SFAFGGNSG	ILLSSLDSP	ETLPARENLK
msa118713.2{361_M781}	PENFVYHQKR	EYPIRNALNF	SFAFGGNSG	ILLSSLDSP	ETLPARENLK

Table 75: Comparative Sequences relating to SAG0671

msa118713.2{361_18RS21}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK		
msa118713.2{361_A909}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK		
msa118713.2{361_COH1}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK		
msa118713.2{361_H36B}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK		
msa118713.2{361_JM9130013}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK		
msa118713.2{361_M732}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK		
msa118713.2{GBS361_2603}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK		
Consensus	*****	*****	*****	*****	*****		
msa118713.2{361_090}	401	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR	450
msa118713.2{361_1169NT}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR		
msa118713.2{361_CJB110}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR		
msa118713.2{361_M781}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR		
msa118713.2{361_18RS21}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR		
msa118713.2{361_A909}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR		
msa118713.2{361_COH1}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR		
msa118713.2{361_H36B}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR		
msa118713.2{361_JM9130013}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR		
msa118713.2{361_M732}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR		
msa118713.2{GBS361_2603}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR		
Consensus	*****	*****	*****	*****	*****		
msa118713.2{361_090}	451	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTSL	GPVEVVEGIE	500
msa118713.2{361_1169NT}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTSL	GPVEVVEGIE		
msa118713.2{361_CJB110}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTSL	GPVEVVEGIE		
msa118713.2{361_M781}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTSL	GPVEVVEGIE		
msa118713.2{361_18RS21}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTSL	GPVEVVEGIE		
msa118713.2{361_A909}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTSL	GPVEVVEGIE		
msa118713.2{361_COH1}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTSL	GPVEVVEGIE		
msa118713.2{361_H36B}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTSL	GPVEVVEGIE		
msa118713.2{361_JM9130013}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTSL	GPVEVVEGIE		
msa118713.2{361_M732}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTSL	GPVEVVEGIE		
msa118713.2{GBS361_2603}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTSL	GPVEVVEGIE		
Consensus	*****	*****	*****	*****	*****		
msa118713.2{361_090}	501	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG	550
msa118713.2{361_1169NT}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG		
msa118713.2{361_CJB110}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG		
msa118713.2{361_M781}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG		
msa118713.2{361_18RS21}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG		
msa118713.2{361_A909}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG		
msa118713.2{361_COH1}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG		
msa118713.2{361_H36B}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG		
msa118713.2{361_JM9130013}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG		
msa118713.2{361_M732}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG		
msa118713.2{GBS361_2603}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG		
Consensus	*****	*****	*****	*****	*****		
msa118713.2{361_090}	551	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGSDYCSA	600
msa118713.2{361_1169NT}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGSDYCSA		
msa118713.2{361_CJB110}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGSDYCSA		
msa118713.2{361_M781}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGSDYCSA		
msa118713.2{361_18RS21}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGSDYCSA		
msa118713.2{361_A909}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGSDYCSA		
msa118713.2{361_COH1}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGSDYCSA		
msa118713.2{361_H36B}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGSDYCSA		
msa118713.2{361_JM9130013}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGSDYCSA		
msa118713.2{361_M732}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGSDYCSA		
msa118713.2{GBS361_2603}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGSDYCSA		
Consensus	*****	*****	*****	*****	*****		
msa118713.2{361_090}	601	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTIK	650
msa118713.2{361_1169NT}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTIK		
msa118713.2{361_CJB110}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTIK		
msa118713.2{361_M781}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTIK		
msa118713.2{361_18RS21}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTIK		
msa118713.2{361_A909}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTIK		
msa118713.2{361_COH1}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTIK		
msa118713.2{361_H36B}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTIK		
msa118713.2{361_JM9130013}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTIK		
msa118713.2{361_M732}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTIK		
msa118713.2{GBS361_2603}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTIK		
Consensus	*****	*****	*****	*****	*****		
msa118713.2{361_090}	651	DIKGFVWNER	KKAVSSDYDF	LANLSEYNYM	PNLASGQFGF	SSNGAGEELD	700
msa118713.2{361_1169NT}	DIKGFVWNER	KKAVSSDYDF	LANLSEYNYM	PNLASGQFGF	SSNGAGEELD		
msa118713.2{361_CJB110}	DIKGFVWNER	KKAVSSDYDF	LANLSEYNYM	PNLASGQFGF	SSNGAGEELD		

Table 75: Comparative Sequences relating to SAG0671

msa118713.2{361_M781}	DIKGFVWNER	KKAVSSDYDF	LANLSEYNYM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_18RS21}	DIKGFVWNER	KKAVSSDYDF	LANLSEYNYM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_A909}	DIKGFVWNER	KKAVSSDYDF	LANLSEYNYM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_COH1}	DIKGFVWNER	KKAVSSDYDF	LANLSEYNYM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_H36B}	DIKGFVWNER	KKAVSSDYDF	LANLSEYNYM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_JM9130013}	DIKGFVWNER	KKAVSSDYDF	LANLSEYNYM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_M732}	DIKGFVWNER	KKAVSSDYDF	LANLSEYNYM	PNLASGQFGF	SSNGAGEELD
msa118713.2{GBS361_2603}	DIKGFVWNER	KKAVSSDYDF	LANLSEYNYM	PNLASGQFGF	SSNGAGEELD
Consensus	*****	*****	*****	*****	*****
	701			731	
msa118713.2{361_090}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_1169NT}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_CJB110}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_M781}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_18RS21}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_A909}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_COH1}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_H36B}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_JM9130013}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_M732}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{GBS361_2603}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
Consensus	*****	*****	*****	*	

Table 76: Comparative Sequences relating to SAG0260

SEQ ID NO. 7601

STRAIN 2603

ATGAAAAAAGTCATCGATTAAAAAACTACAAAAAGCATATGCCTCAGAAACCGTTTAA
 AATAATATTAAATTGGAGGTGTTTAAAGGCGAAATAATTGGATTAAATAGGACCCCTCTGGA
 GCAGGGAATCTACCTTGATTAAAACTATGCTTGGCATGAAAAAGCAGATAAGGGAACA
 GCTCTTGTCTTGATACCTCAAATGCCAGATCGTAATATTTTAAATCAAATGGCTATATG
 GCTCAATCTGATGCCTTATACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCTTTGGA
 AAAATGAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATAACTCATATTTCTAAAGTA
 GTAGATCTAGAAAAACCACTTGATAAATTTGTCTCAGGTTACTCAGGAGGTATGAAAAA
 CGGCTTTCTCTAGCCATCGCCCTACTTGGAAACCCACAGTTTAACTCTAGATGAACCT
 ACCGTTGGAATTGATCCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAG
 GATGAAGACATTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAATTAACAAGT
 AAGGTGCACTACTATTACGTGGAACATTATTGCCCTTGATACTCCATTACATTTAAAA
 AAACAATTTAATGTGAGTACTATTGAGGAAGTTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7602

STRAIN 090

ATTTAAAAAACTACAAAAAGCATATGCCTCAGAAACTGTTTTTAAATAAT
 ATTAATTTGGAGGTGTTTAAAGGCGAAATAATTGGATTAAATAGGACCCCTC
 TGGAGCAGGGAATCTACCTTGATTAAAACTATGCTTGGCATGAAAAAG
 CAGATAAGGGAACAGCTCTTGTCTTGATACTCAAATGCCAGATCGTAAT
 ATTTTAAATCAAATTGGCTATATGGCTCAATCTGATGCCTTATACGAATC
 TTTAACTGCCCTAGAAATTTATTATTCTTTGGAAAAATGAAAGGTATTCT
 AAAAACTGAATTAAAAACAGCAGATAACTCATATTTCTAAAGTAGTAGAT
 CTAGAAAAACCACTTGATAAATTTGTCTCAGGTTACTCAGGAGGTATGAA
 AAGACGGCTTTCTCTAGCCATCGCCCTACTTGGAAACCCACAGTTTAA
 TCCTAGATGAACCTACCGTTGGAATTGATCCATCCTTGAGGAGAAAAATC
 TGGCAAGAGCTAATTAATATTAAAGGATGAAGGACGTTCTATCTTTATTAC
 AACCCACGTTATGGATGAAGCAGAAATTAACAAGTAAGGTTGCACTACTAT
 TACGTGGAACATTATTGCCCTTGATACTCCATTACATTTAAAAAAACAA
 TTTAATGTGAGTACTATTGAGGAAGTTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7603

STRAIN A909

AAAAAAGTCATCGATTAAAAAACTACAAAAAGCATATGCCTCA
 GAAACCGTTTTTAAATAATATTAAATTTGGAGGTGTTTAAAGGCGAAATAAT
 TGGATTAAATAGGACCCCTCTGGAGCAGGGAATCTACCTTGATTAAAACTA
 TGCTTGGCATGAAAAAGCAGATAAGGGAACAGCTCTTGTCTTGATACT
 CAAATGCCAGATCATAATATTTTAAATCAAATTGGCTATATGGCTCAATC
 TGATGCCCTTATACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCTTTG
 GAAAAATGAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATAACTCAT
 ATTTCTAAAGTAGTAGATCTAGAAAAACCACTTGATAAATTTGTCTCAGG
 TTAATCAGGAGGTATGAAAAAGACGGCTTTCTCTAGCCATCGCCCTACTTG
 GAAACCCACAGTTTTAATCTAGATGAACCTACCGTTGGAATTGATCCA
 TCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAAGGATGAAGG
 ACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAATTAACAA
 GTAAGGTTGCACTACTATTACGTGGAACATTATTGCCCTTGATACTCCA
 TTACATTTAAAAAAACAAATTTAATGTGAGTACTATTGAGGAAGTTTTCTT
 AAAAGCTGAAGGAGAA

SEQ ID NO. 7604

STRAIN H36B

AAAAAAGTCATTGATTAAAAAACTACAAAAAGCATATGCC
 TCAGAAACCGTTTTTAAATAATATTAAATTTGGAGGTGTTTAAAGGCGAAAT
 AATTGGATTAAATAGGACCCCTCTGGAGCAGGGAATCTACCTTGATTAAAA
 CTATGCTTGGCATGAAAAAGCAGATAAGGGAACAGCTCTTGTCTTGAT
 ACTCAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGCTCA
 ATCTGATGCCCTTATACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCT
 TTGAAAAATGAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATAACT
 CATATTTCTAAAGTAGTAGATCTAGAAAAACCACTTGATAAATTTGTCTC
 AGGTTACTCAGGAGGTATGAAAAAGACGGCTTTCTCTAGCCATCGCCCTAC
 TTGAAAAACCCACAGTTTTAATCTAGATGAACCTACCGTTGGAATTGAT
 CCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAAGGATGA
 AGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAATTA
 CAAGTAAGGTTGCACTACTATTACGTGGAACATTATTGCCCTTGATACT
 CCATTACATTTAAAAAAACAAATTTAATGTGAGTACTATTGAGGAAGTTTT
 CTTAAAGCTGAAGGAGAA

SEQ ID NO. 7605

STRAIN 18RS21

GATTTAAAAAACTACAAAAAGCATATGCCTCAGAAACCGTTTTTAAATAA
 TATTAAATTTGGAGGTGTTTAAAGGCGAAATAATTGGATTAAATAGGACCCCT
 CTGGAGCAGGGAATCTACCTTGATTAAAACTATGCTTGGCATGAAAAA
 GCAGATAAGGGAACAGCTCTTGTCTTGATACTCAAATGCCAGATCGTA
 TATTTTAAATCAAATTGGCTATATGGCTCAATCTGATGCCTTATACGAGT
 CTTTAACTGGCTTAGAAAAATTTATTATTCTTTGAAAAATGAAAGGTATT
 CAAAAACCTGAATTAAAAACAGCAGATAACTCATATTTCTAAAGTAGTAGA
 TCTAGAAAAACCACTTGATAAATTTGTCTCAGGTTACTCAGGAGGTATGA
 AAGACGGCTTTCTCTAGCCATCGCCCTACTTGGAAACCCACAGTTTAA
 ATCTAGATGAACCTACCGTTGGAATTGATCCATCCTTGAGGAGAAAAAT
 CTGGCAAGAGCTAATTAATATTAAAGGATGAAGGACATTTCTATCTTTATTA
 CAACCCACGTTATGGATGAAGCAGAAATTAACAAGTAAGGTTGCACTACTA

Table 76: Comparative Sequences relating to SAG0260

TTACGTGGAACATTATTGCCCTTGATACTCCATTACATTAAAAAACA
ATTTAATGTGAGTACTATTGAGGAAGTTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7606

STRAIN M732

AAAAAAGTCATCGATTAAAAAACTACAAAAAGCATACGCCTCA
GAACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGAGAAATAAT
TGGATTAAATAGGACCCTCTGGAGCAGGGAATCTACCTTGATTAAAACTA
TGCTTGGCATGAAAAAGCAGATAAGGGAACAGCTCTTGTTCTTGATACT
CAAATGCCAGATCGTAATTTTAAATCAAATGGCTATATGGCTCAATC
TGATGCCCTTACACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCTTG
GAAAAATGAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATAACTCAT
ATTTCTAAAGTAGTAGATCTAGAAAACCACTTGATAAATTTGTCCTCAGG
TTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTACTTG
GAAACCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTGATCCA
TCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAAGGATGAAGG
ACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTAAACA
GTAAGGTGCACTACTATTACGTGGAACATTATTGCCTTTGATACTCCA
TTACATTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAGTTTCTT
AAAAGCTGAAGGAGAA

SEQ ID NO. 7607

STRAIN COH1

AAAAAAGTCATCGATTAAAAAACTACAAAAAGCATACGCCTCAGAA
ACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGAGAAATAATGG
ATTAATAGGACCCTCTGGAGCAGGGAATCTACCTTGATTAAAACTATGC
TTGGCATGGAATAAGCAGATAAGGGAACAGCTCTTGTTCTTGATACTCAA
ATGCCAGATCGTAATTTTAAATCAAATGGCTATATGGCTCAATCTGA
TGCTTTACACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCTTGGA
AATGAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATAACTCATATT
TCTAAAGTAGTAGATCTAGAAAACCACTTGATAAATTTGTCCTCAGGTTA
CTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTACTTGGA
ACCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTGATCCATCC
TTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAAGGATGAAGGAG
TTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTAAACAAGTA
AGGTTGCACTACTATTACGTGGAACATTATTGCCTTTGATACTCCATTA
CAITTAATAAAACAATTTAATGTGAGTACTATTGAGGAAG

SEQ ID NO. 7608

STRAIN M781

AAAAAAGTCATCGATTAAAAAACTACAAAAAGCATAC
GCCTCAGAACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGAGA
AATAATTGGATTAAATAGGACCCTCTGGAGCAGGGAATCTACCTTGATTAA
AACTATGCTTGGCATGGAATAAGCAGATAAGGGAACAGCTCTTGTTCTT
GATACTCAAATGCCAGATCGTAATTTTAAATCAAATGGCTATATGGC
TCAATCTGATGCCCTTACACGAGTCTTTAACTGGCTTAGAAAAATTTATTAT
TCTTTGGAATAAGTAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATA
ACTCATATTTCTAAAGTAGTAGATCTAGAAAACCACTTGATAAATTTGT
CTCAGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCC
TACTTGGAACCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATT
GATCCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAAGGA
TGAAGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAT
TAACAAGTAAGGTGCACTACTATTACGTGGAACATTATTGCCTTTGAT
ACTCCATTACATTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAGT
TTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7609

STRAIN CJB110

AAAAAAGTCATCGATTAAAAAACTACAAAAAGCATATG
CCTCAGAACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGCGAA
ATAATTGGATTAAATAGGACCCTCTGGAGCAGGGAATCTACCTTGATTAA
AACTATGCTTGGCATGGAATAAGCAGATAAGGGAACAGCTCTTGTTCTTG
ATACTCAAATGCCAGATCGTAATTTTAAATCAAATGGCTATATGGCT
CAATCTGATGCCCTTATACGAATCTTTAACTGCCCTAGAAAAATTTATTATT
CTTTGGAATAAGTAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATAA
CTCATATTTCTAAAGTAGTAGATCTAGAAAACCACTTGATAAATTTGTC
TCAGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCT
ACTTGGAACCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTG
ATCATCTCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAAGGAT
GAAGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAT
AACAAGTAAGGTGCACTACTATTACGTGGAACATTATTGCCTTTGATA
CTCCATTACATTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAGTT
TTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7610

STRAIN 1169NT

AAAAAAGTCATCGATTAAAAAACTACAAAAAGCATAC
GCCTCAGAACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGCGA
AATAATTGGATTAAATAGGACCCTCTGGAGCAGGGAATCTACCTTGATTAA
AACTATGCTTGGCATGGAATAAGCAGATAAGGGAACAGCTCTTGTTCTT
GATACTCAAATGCCAGATCGTAATTTTAAATCAAATGGCTATATGGC
TCAATCTGATGCCCTTATACGAATCTTTAACTGCCCTAGAAAAATTTATTAT

Table 76: Comparative Sequences relating to SAG0260

TCCTTGGAAAAATGAAAGGTATTCAAAAACTGAATTAACAGCAGATA
 ACTCATATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGT
 CTCAGGTTACTCAGGAGGTATGAAAAGACGGCTTCTCTAGCCATCGCCC
 TACTTGGAAACCCACAGTTTAAATCCTAGATGAACCTACCGTTGGAATT
 GATCCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATTAAGGA
 TGAAGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAT
 TAACAAGTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGAT
 ACTCCATTACATTTAAAAAAACAATTAATGTGAGTACTATTGAGGAAGT
 TTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7611

STRAIN JM9130013

AAAAAGTCATCGATTTAAAAAACTACAAAAGCATATGCC
 TCAGAAACCGTTTAAATAATTAATTTGGAGGTGTTTAAAGGCGAAAT
 AATTTGGATTAATAGGACCTCTGGAGCAGGGAATCTACCTTGATTAAAA
 CTATGCTTGGCATGGAAAAAGCAGATAAGGGAACAGCTCTTGTTCCTGAT
 ACTCAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGCTCA
 ATCTGATGCCTTATACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCT
 TTGGAATAATGAAAGGTATTCAAAAACTGAATTAACAGCAGATAAAT
 CATATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTCTC
 AGGTTACTCAGGAGGTATGAAAAGACGGCTTCTCTAGCCATCGCCCTAC
 TTGGAACCCACAGTTTAAATCCTAGATGAACCTACCGTTGGAATTGAT
 CCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATTAATAGGATGA
 AGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTA
 CAAGTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGATACT
 CCATTACATTTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAGTTT
 CTTAAAAAGCTGAAGGAGAA

PRETTY of: /biotmp/msa134270.2{*} April 10, 2003 02:14 ..

	1				50
msa134270.2{391_COH1}	-----aaaaaag	tcacgcgATTT	AAAAAACTA	CAAAAAGCAT	AcGCCTCAGA
msa134270.2{391_M732}	-----aaaaaag	tcacgcgATTT	AAAAAACTA	CAAAAAGCAT	AcGCCTCAGA
msa134270.2{391_M781}	-----aaaaaag	tcacgcgATTT	AAAAAACTA	CAAAAAGCAT	AcGCCTCAGA
msa134270.2{391_090}	-----	-----ATTT	AAAAAACTA	CAAAAAGCAT	AtGCCTCAGA
msa134270.2{391_CJB110}	-----aaaaaag	tcacgcgATTT	AAAAAACTA	CAAAAAGCAT	AtGCCTCAGA
msa134270.2{391_1169NT}	-----aaaaaag	tcacgcgATTT	AAAAAACTA	CAAAAAGCAT	AcGCCTCAGA
msa134270.2{391_18RS21}	-----	-----gATTT	AAAAAACTA	CAAAAAGCAT	AtGCCTCAGA
msa134270.2{391_2603}	atgaaaaaag	tcacgcgATTT	AAAAAACTA	CAAAAAGCAT	AtGCCTCAGA
msa134270.2{391_A909}	-----aaaaaag	tcacgcgATTT	AAAAAACTA	CAAAAAGCAT	AtGCCTCAGA
msa134270.2{391_JM9130013}	-----aaaaaag	tcacgcgATTT	AAAAAACTA	CAAAAAGCAT	AtGCCTCAGA
msa134270.2{391_H36B}	-----aaaaaag	tcattgATTT	AAAAAACTA	CAAAAAGCAT	AtGCCTCAGA
Consensus	***-----	-----****	*****	*****	*-*****

	51				100
msa134270.2{391_COH1}	AACtGTTTTA	AATAATATTA	ATTGAGGT	GTTTAAAGGa	GAAATAATTG
msa134270.2{391_M732}	AACtGTTTTA	AATAATATTA	ATTGAGGT	GTTTAAAGGa	GAAATAATTG
msa134270.2{391_M781}	AACtGTTTTA	AATAATATTA	ATTGAGGT	GTTTAAAGGa	GAAATAATTG
msa134270.2{391_090}	AACtGTTTTA	AATAATATTA	ATTGAGGT	GTTTAAAGGc	GAAATAATTG
msa134270.2{391_CJB110}	AACtGTTTTA	AATAATATTA	ATTGAGGT	GTTTAAAGGc	GAAATAATTG
msa134270.2{391_1169NT}	AACtGTTTTA	AATAATATTA	ATTGAGGT	GTTTAAAGGc	GAAATAATTG
msa134270.2{391_18RS21}	AACcGTTTTA	AATAATATTA	ATTGAGGT	GTTTAAAGGc	GAAATAATTG
msa134270.2{391_2603}	AACcGTTTTA	AATAATATTA	ATTGAGGT	GTTTAAAGGc	GAAATAATTG
msa134270.2{391_A909}	AACcGTTTTA	AATAATATTA	ATTGAGGT	GTTTAAAGGc	GAAATAATTG
msa134270.2{391_JM9130013}	AACcGTTTTA	AATAATATTA	ATTGAGGT	GTTTAAAGGc	GAAATAATTG
msa134270.2{391_H36B}	AACcGTTTTA	AATAATATTA	ATTGAGGT	GTTTAAAGGc	GAAATAATTG
Consensus	***-*****	*****	*****	*****	*****

	101				150
msa134270.2{391_COH1}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_M732}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_M781}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_090}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_CJB110}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_1169NT}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_18RS21}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_2603}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_A909}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_JM9130013}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_H36B}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
Consensus	*****	*****	*****	*****	*****

	151				200
msa134270.2{391_COH1}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_M732}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_M781}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_090}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_CJB110}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_1169NT}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_18RS21}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_2603}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_A909}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA

Table 76: Comparative Sequences relating to SAG0260

msa134270.2{391_JM9130013}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_H36B}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
Consensus	*****	*****	*****	*****	*****
	201				250
msa134270.2{391_COH1}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_M732}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_M781}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_090}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_CJB110}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_1169NT}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_18RS21}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_2603}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_A909}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_JM9130013}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_H36B}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
Consensus	*****	*-*****	*****	*****	*****
	251				300
msa134270.2{391_COH1}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_M732}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_M781}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_090}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_CJB110}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_1169NT}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_18RS21}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_2603}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_A909}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_JM9130013}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_H36B}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
Consensus	*****-*	***-*****	****-*****	*****	*****
	301				350
msa134270.2{391_COH1}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_M732}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_M781}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_090}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_CJB110}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_1169NT}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_18RS21}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_2603}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_A909}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_JM9130013}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_H36B}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
Consensus	*****	*****	*****	*****	*****
	351				400
msa134270.2{391_COH1}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_M732}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_M781}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_090}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_CJB110}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_1169NT}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_18RS21}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_2603}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_A909}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_JM9130013}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_H36B}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
Consensus	*****	*****	*****	*****	*****
	401				450
msa134270.2{391_COH1}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_M732}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_M781}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_090}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_CJB110}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_1169NT}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_18RS21}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_2603}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_A909}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_JM9130013}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_H36B}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
Consensus	*****	*****	*****	*****	*****
	451				500
msa134270.2{391_COH1}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_M732}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_M781}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_090}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_CJB110}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_1169NT}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_18RS21}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_2603}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC

Table 76: Comparative Sequences relating to SAG0260

msa134270.2{391_A909}	AACCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_JM9130013}	AACCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_H36B}	AACCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
Consensus	*****	*****	*****	*****	*****
501					
msa134270.2{391_COH1}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_M732}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_M781}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_090}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_CJB110}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_1169NT}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_18RS21}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_2603}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_A909}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_JM9130013}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_H36B}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
Consensus	*****	*****	*****	*****	*****
551					
msa134270.2{391_COH1}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_M732}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_M781}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_090}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_CJB110}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_1169NT}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_18RS21}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_2603}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_A909}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_JM9130013}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_H36B}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
Consensus	*****	*****	*****	*****	*****
601					
msa134270.2{391_COH1}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_M732}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_M781}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_090}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_CJB110}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_1169NT}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_18RS21}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_2603}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_A909}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_JM9130013}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_H36B}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
Consensus	*****	*****	*****	*****	*****
651					
msa134270.2{391_COH1}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	G-----
msa134270.2{391_M732}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_M781}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_090}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_CJB110}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_1169NT}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_18RS21}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_2603}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_A909}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_JM9130013}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_H36B}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
Consensus	*****	*****	*****	*****	*****
701					
msa134270.2{391_COH1}	-----	714			
msa134270.2{391_M732}	AAGCTGAAGG	AGAA			
msa134270.2{391_M781}	AAGCTGAAGG	AGAA			
msa134270.2{391_090}	AAGCTGAAGG	AGAA			
msa134270.2{391_CJB110}	AAGCTGAAGG	AGAA			
msa134270.2{391_1169NT}	AAGCTGAAGG	AGAA			
msa134270.2{391_18RS21}	AAGCTGAAGG	AGAA			
msa134270.2{391_2603}	AAGCTGAAGG	AGAA			
msa134270.2{391_A909}	AAGCTGAAGG	AGAA			
msa134270.2{391_JM9130013}	AAGCTGAAGG	AGAA			
msa134270.2{391_H36B}	AAGCTGAAGG	AGAA			
Consensus	*****	***			

SEQ ID NO. 7612

STRAIN 2603 frame: 1

KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKMLGMEKADKGTALVLDTPMPDRNINLQIGYMAQSDALYESLTGLENLFFGKMKGIQKTELKQIITHISKVVDLENQLDKFVSGYSGGKMRRLSLATALLGNPTVLILDEPTVGIDPSLRRIKIQWELINKDEGHSIFITTHVDEAELTSKVALLLRGNTIAFDTPHLKQFNV

SEQ ID NO. 7613

Table 76: Comparative Sequences relating to SAG0260

STRAIN 090 frame: 3
 LKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGTALVLD
 QMPDRNINLQIGYMAQSDALYESLTALENLLFFGKMKGIQKTELKQIITHISKVVDLENQ
 LDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRIWQELINIKDEGRSI
 FITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7614

STRAIN A909 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7615

STRAIN H36B frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7616

STRAIN 18RS21 frame: 1
 DLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGTALVLD
 TQMPDRNINLQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQIITHISKVVDLEN
 QDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRIWQELINIKDEGHS
 IFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7617

STRAIN M732 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALHESLTGLENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7618

STRAIN COH1 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALHESLTGLENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7619

STRAIN M781 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALHESLTGLENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7620

STRAIN CJB110 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALYESLTALENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7621

STRAIN 1169NT frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALYESLTALENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7622

STRAIN JM9130013 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

PRETTY of: /biotmp/msa134470.2{*} April 10, 2003 02:16 ..

	1	50
msa134470.2{391_090}	-----LKKLQ KAYASETVLN NINLEVFKEI IGLIGPSGA GKSTLIKTM	
msa134470.2{391_1169NT}	KKVIDLKKLQ KAYASETVLN NINLEVFKEI IGLIGPSGA GKSTLIKTM	
msa134470.2{391_CJB110}	KKVIDLKKLQ KAYASETVLN NINLEVFKEI IGLIGPSGA GKSTLIKTM	
msa134470.2{391_COH1}	KKVIDLKKLQ KAYASETVLN NINLEVFKEI IGLIGPSGA GKSTLIKTM	
msa134470.2{391_M732}	KKVIDLKKLQ KAYASETVLN NINLEVFKEI IGLIGPSGA GKSTLIKTM	
msa134470.2{391_M781}	KKVIDLKKLQ KAYASETVLN NINLEVFKEI IGLIGPSGA GKSTLIKTM	
msa134470.2{391_18RS21}	-----DLKKLQ KAYASETVLN NINLEVFKEI IGLIGPSGA GKSTLIKTM	
msa134470.2{391_2603}	KKVIDLKKLQ KAYASETVLN NINLEVFKEI IGLIGPSGA GKSTLIKTM	
msa134470.2{391_H36B}	KKVIDLKKLQ KAYASETVLN NINLEVFKEI IGLIGPSGA GKSTLIKTM	
msa134470.2{391_JM9130013}	KKVIDLKKLQ KAYASETVLN NINLEVFKEI IGLIGPSGA GKSTLIKTM	

Table 76: Comparative Sequences relating to SAG0260

msa134470.2{391_A909}	KKVIDLKKLQ	KAYASETVLN	NINLEVFKE	IIGLIGPSGA	GKSTLIKTML
Consensus	*****	*****	*****	*****	*****
	51				100
msa134470.2{391_090}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	aLENLLFFGK
msa134470.2{391_1169NT}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	aLENLLFFGK
msa134470.2{391_CJB110}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	aLENLLFFGK
msa134470.2{391_COH1}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALhESLT	gLENLLFFGK
msa134470.2{391_M732}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALhESLT	gLENLLFFGK
msa134470.2{391_M781}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALhESLT	gLENLLFFGK
msa134470.2{391_18RS21}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	gLENLLFFGK
msa134470.2{391_2603}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	gLENLLFFGK
msa134470.2{391_H36B}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	gLENLLFFGK
msa134470.2{391_JM9130013}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	gLENLLFFGK
msa134470.2{391_A909}	GMEKADKGTA	LVLDTQMPDh	NILNQIGYMA	QSDALyESLT	gLENLLFFGK
Consensus	*****	*****	*****	*****	*****
	101				150
msa134470.2{391_090}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_1169NT}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_CJB110}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_COH1}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_M732}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_M781}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_18RS21}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_2603}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_H36B}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_JM9130013}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_A909}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
Consensus	*****	*****	*****	*****	*****
	151				200
msa134470.2{391_090}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_1169NT}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_CJB110}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_COH1}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_M732}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_M781}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_18RS21}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGhSIFITTH	VMDEAELTSK
msa134470.2{391_2603}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGhSIFITTH	VMDEAELTSK
msa134470.2{391_H36B}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_JM9130013}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_A909}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
Consensus	*****	*****	*****	*****	*****
	201		224		
msa134470.2{391_090}	VALLLRGNII	AFDTPHLKK	QFNV		
msa134470.2{391_1169NT}	VALLLRGNII	AFDTPHLKK	QFNV		
msa134470.2{391_CJB110}	VALLLRGNII	AFDTPHLKK	QFNV		
msa134470.2{391_COH1}	VALLLRGNII	AFDTPHLKK	QFNV		
msa134470.2{391_M732}	VALLLRGNII	AFDTPHLKK	QFNV		
msa134470.2{391_M781}	VALLLRGNII	AFDTPHLKK	QFNV		
msa134470.2{391_18RS21}	VALLLRGNII	AFDTPHLKK	QFNV		
msa134470.2{391_2603}	VALLLRGNII	AFDTPHLKK	QFNV		
msa134470.2{391_H36B}	VALLLRGNII	AFDTPHLKK	QFNV		
msa134470.2{391_JM9130013}	VALLLRGNII	AFDTPHLKK	QFNV		
msa134470.2{391_A909}	VALLLRGNII	AFDTPHLKK	QFNV		
Consensus	*****	*****	****		

Table 77: Comparative Sequences relating to SAG2059

SEQ ID NO. 7701

STRAIN 2603

TTGCCTATGTTGCTCTGTTGGTTTAGTTTTAGAGGGTGGCGGAATGAGAGGTCTTTATACT
GCTGGAGTTTTAGATGCTTTTCTAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGTC
TCTGCTGCTGCTGCTGTTTGGTGGTTAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGA
TACAATAAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGGTTTCGAACA
GGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTCCTATGAAATGGATGTATTT
GACGATGAAGCATTTAAAAAATCAAGTATGATTTTTACGTAGTTGCTACAGAGATGACA
TCTGGTAAACCTGAATATTTTAAATTTGATAGTGTTTTTGAACAAATGGAATTTTACGT
GCTAGTTGAGCATTACAGTAGTCTCAAGATGGTTGATTGGCAGGGGAAAAAGTACTTA
GATGGTGGTTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGATTGACAAG
TTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGCCTCAAGTGGACGATTG
TATAAACTCTGTATAGGAAATATCCTAATTTTGTAAAGACAGCCTCGAATCGGTACCAA
CAGTATAATAATAGTCTTGAAAAGGTCTAGAGCCTTGAAAAAACAGGCGATCTATTTGCA
ATTAGACCGAGTAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGAT
AGTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCTGAATAGTTAT
CTAATGAAA

SEQ ID NO. 7702

STRAIN 090

CCTATGTTGCTCTGTTGGTTTAGTTTTAG
AGGGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTTT
CTAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGCTCTGCTGGTGC
ATTGTTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGAT
ACAATAAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGG
TTTCGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTC
TATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTG
ATTTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTT
AAAATTGATAGTGTTTTTGAACAAATGGAATTTTACGTGCTAGTTTCAGC
ATTACAGTAGTCTCAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAG
ATGGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGA
TTTGACAAGTTGATTTGTGTGATGACTAGGCCGCTCAATTATCAGAAAAA
GCCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATT
TTGTAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAA
AAGGTCATGAGCCTTGAAAAAACAGGCGATCTATTTGCAATTAGACCGAG
TAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATA
GTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCTG
AATAGTTATCTAATGAAA

SEQ ID NO. 7703

STRAIN A909

CCTATGTTGCTCTGTTGGTTTAGTTTTAGAG
GGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTTTCT
AGATGCAGGAATAAAAGTAGATGGTATCATATCTGCTCTGCTGGTGCAT
TGTTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATAC
AATAAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGGCT
TCGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTCCTA
TGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGAT
TTTTACGAGTTGCTACAGAGATGACATCTGGTAAACCTGAGTATTTTAA
AATTGATAGTGTTTTTGAACAAATGGAATTTTACGTGCTAGTTTCAGCAT
TACCAGTAGTCTCAAGATGGTTGTTTGGCAGGGGAAAAAGTACTTAGAT
GGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGAT
TGACAAGTTGATTTGTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGC
CTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTT
GTAAAGACAGCCTCGAACCCTGACCAACAGTATAATAATAGCCTTGAAAA
GGTCATGAGCCTTGAAAAAACAGGCGATCTATTTGCAATTAGACCAAGTA
AGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAGT
ATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGGGATGCCTGAGCTGAA
TAGTTATCTAATGAAA

SEQ ID NO. 7704

STRAIN H36B

CCTATGTTGCTCTGTTGGTTTAGTTTTAG
AGGGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTTT
CTAGATGCAGGAATAAAAGTAGATGGTATCATATCTGCTCTGCTGGTGC
ATTGTTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGAT
ACAATAAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGG
CTTCGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTCCTA
TATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTG
ATTTTTACGAGTTGCTACAGAGATGACATCTGGTAAACCTGAGTATTTT
AAAATTGATAGTGTTTTTGAACAAATGGAATTTTACGTGCTAGTTTCAGC
ATTACAGTAGTCTCAAGATGGTTGTTTGGCAGGGGAAAAAGTACTTAG
ATGGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGA
TTTGACAAGTTGATTTGTGTGATGACTAGGCCGCTCAATTATCAGAAAAA
GCCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATT
TTGTAAAGACAGCCTCGAACCCTGACCAACAGTATAATAATAGCCTTGAA
AAGGTCATGAGCCTTGAAAAAACAGGCGATCTATTTGCAATTAGACCAAG
TAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATA
GTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGGGATGCCTGAGCTG
AATAGTTATCTAATGAAA

SEQ ID NO. 7705

Table 77: Comparative Sequences relating to SAG2059

STRAIN 18RS21

CCTATGTTGTCGTGGTTTGTAGTTTGTAGAGG
 GTGGCGGAATGAGAGGCTTTTATACTGCTGGAGTTTGTAGATGCTTTTCTA
 GATGCAGGAATAAAAAATAGATGGTATCGTATCTGTCTCTGCTGGTGCATT
 GTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATACA
 ATAAAAAGTATTTATCCCAACCCTAAATATATGAGTCTAAGGTCATGGTTT
 CGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTCCTAT
 GAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGATT
 TTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTTAAA
 ATTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTTCAAGCATT
 ACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAGATG
 GTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGATTT
 GACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGCC
 TTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTTG
 TAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAAAAG
 GTCATGAGCCTTGAAAAACAGCGCATCTATTGCAATTAGACCGAGTAA
 GAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAGTA
 TTTATCAGCTTGGTATGAAAAGATGCTAAAAGTGTGATGCCTGAGCTGAAT
 AGTTATCTAATGAAA

SEQ ID NO. 7706

STRAIN M732

CCTATGTTGTCGTGGTTTGTAGTTTGTAGA
 GGGTGGCGGAATGAGAGGCTTTTATACTGCTGGAGTTTGTAGATGCTTTTC
 TAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTGCA
 TTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATA
 CAATAAAAAGTATTTATCCCAACCCTGAATATATGAGTCTAAGATCATGGC
 TTCGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTCCT
 ATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGA
 TTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTTA
 AAATTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTTCAAGCA
 TTACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAGA
 TGGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGAT
 TTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAG
 CCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTT
 TGTAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAAA
 AGGTCATGAGCCTTGAAAAACAGCGCATCTATTGCAATTAGACCGAGT
 AAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAG
 TATTATCAGCTTGGTATGAAAATATGCTAAAAGTGTGATGCCTGAGCTGA
 ATAGTTATCTAATGAAA

SEQ ID NO. 7707

STRAIN COH1

CCTATGTTGTCGTGGTTTGTAGTTTGA
 GAGGTGGCGGAATGAGAGGCTTTTATACTGCTGGAGTTTGTAGATGCTTT
 TCTAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTG
 CATTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGA
 TACAATAAAAAGTATTTATCCCAACCCTGAATATATGAGTCTAAGATCATG
 GCTTCGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTC
 CTATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATT
 GATTTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTT
 TAAATTTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTTCAAG
 CATTACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTA
 GATGGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGG
 ATTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAA
 AGCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAAT
 TTTGTAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGA
 AAAGTTCATGAGCCTTGAAAAACAGCGCATCTATTGCAATTAGACCGA
 GTAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGAT
 AGTATTTATCAGCTTGGTATGAAAATATGCTAAAAGTGTGATGCCTGAGCT
 GAATAGTTATCTAATGAAA

SEQ ID NO. 7708

STRAIN M781

CCTATGTTGTCGTGGTTTGTAGTTTGTAG
 AGGTGGCGGAATGAGAGGCTTTTATACTGCTGGAGTTTGTAGATGCTTTT
 CTAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTGC
 ATTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGAT
 ACAATAAAAAGTATTTATCCCAACCCTGAATATATGAGTCTAAGATCATGG
 CTTTGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTC
 TATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTG
 ATTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTT
 AAAATTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTTCAAGC
 ATTACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAG
 ATGGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGA
 TTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAA
 GCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAAT
 TTGTAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGA
 AAAGTTCATGAGCCTTGAAAAACAGCGCATCTATTGCAATTAGACCGA
 GTAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGAT
 GTATTTATCAGCTTGGTATGAAAATATGCTAAAAGTGTGATGCCTGAGCTG
 AATAGTTATCTAATGAAA

Table 77: Comparative Sequences relating to SAG2059

SEQ ID NO. 7709

STRAIN CJB110

CCTATGTTGTCGTTGGTTTGTAGTTTAA
 GAGGGTGGCGGAATGAGAGGTCCTTATACCTGCTGGAGTTTGTAGATGCTTT
 TCTAGATGCAGGAATAAAATAGATGGTATCGTATCTGTCTCTGCTGGTG
 CATTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTGC
 TACAATAAAAGATATTATCCCACCCTAAATATATGAGTCTAAGGTCATG
 GTTTCGAACAGGAATTTTGTAAATAAGATTTCACCTATTATGAAGTTC
 CTATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATT
 GATTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTT
 TAAAAATTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTTCA
 CATACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTA
 GATGGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTAGG
 ATTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAA
 AGCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAAT
 TTTGTAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGA
 AAGGTCATGAGCCTTGAAAAAACAGGCGATCTATTGCAATTAGACCGA
 GTAAGAGCTTGGTTATGGCCGCTTAGAGAAGAATCCGGATAAACTTGAT
 AGTATTTATCAGCTTGGTATGAAAGATGCTAAAGTGTGATGCCTGAGCT
 GAATAGTTATCTAATGAAA

SEQ ID NO. 7710

STRAIN 1169NT

CCTATGTTGTCGTTGGTTTGTAGTTTGTAGGGTG
 GCGGAATGAGAGGTCCTTATACCTGCTGGAGTTTGTAGATGCTTTTCTAGAT
 GCAGGAATAAAATAGATGGTATCGTATCTGTCTCTGCGGGTGCATTGTT
 TGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTCGATACAATA
 AAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGATCATGGCTTCGA
 ACAGGGAATTTTGTAAATAAGATTTCACCTATTATGAAGTTCTCTATGAA
 ATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGATTTT
 ACGCAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTTAAAT
 GATAGTGTCTTGAACAAATGGAAATTTTACGTGCTAGTTTCAAGTATACC
 AGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAGATGGTG
 GTTTATCTGATAGTATCCCCTGTTGATTTTGCCCGTGGTTTAGGATTGAC
 AAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGCCTTC
 AAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTTGTAA
 AGACAGCCTCGAATCGGTACCAACAGTATAATAATAGCCTTGAAAGGTC
 ATGAGCCTTGAAAAAACAGGCGATCTATTGCAATTAGGCCGAGTAAAAAG
 CTTGGTTATTGTCGCTTAGAGAAGAATCCGGATAAACTTGATAGTATTT
 ATCAGCTTGGTATGAAAGATGCTAAAGTGTGATGCCTGAGCTGAATAGT
 TATCTAATGAAA

SEQ ID NO. 7711

STRAIN JM9130013

CCTATGTTGTCGTTGGTTTGTAGTTTGTAGAG
 GGTGGCGGAATGAGAGGTCCTTATACCTGCTGGAGTTTGTAGATGCTTTTCT
 AGATGCAGGAATAAAGTAGATGGTATCATATCTGTCTCTGCTGGTGCA
 TGTGTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTCGATAC
 AATAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCTAGGCT
 TCGAACAGGGAATTTTGTAAATAAGATTTCACCTATTATGAAGTTCTCTA
 TGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGAT
 TTTTACGCAGTTGCTACAGAGATGACATCTGGTAAACCTGAGTATTTTAA
 AATTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTTCAAGCAT
 TACCAGTAGTCTCAAAGATGGTTGTTTGGCAGGGGAAAAAGTACTTAGAT
 GGTGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGATT
 TGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGC
 CTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTT
 GTAAAGACAGCCTCGAACCCTGACCAACAGTATAATAATAGCCTTGAAAA
 GGTCTAGAGCCTTGAAAAAACAGGCGATCTATTGCAATTAGACCAAGTA
 AGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAGT
 ATTTATCAGCTTGGTATGAAAGATGCTAAAGTGGGATGCCTGAGCTGAA
 TAGTTATCTAATGAAA

PRETTY of: /biotmp/msa47199.2{*} February 19, 2003 05:51 ..

	1		50
msa47199.2{394_A909}	----CCTATGT	TGTCGTGTTGG	TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_H36B}	----CCTATGT	TGTCGTGTTGG	TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_JM9130013}	----CCTATGT	TGTCGTGTTGG	TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_090}	----CCTATGT	TGTCGTGTTGG	TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_18RS21}	----CCTATGT	TGTCGTGTTGG	TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_2603}	ttgCCTATGT	TGTCGTGTTGG	TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_CJB110}	----CCTATGT	TGTCGTGTTGG	TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_COH1}	----CCTATGT	TGTCGTGTTGG	TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_M732}	----CCTATGT	TGTCGTGTTGG	TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_M781}	----CCTATGT	TGTCGTGTTGG	TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_1169NT}	----CCTATGT	TGTCGTGTTGG	TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
Consensus	*****	*****	*****
	51		100
msa47199.2{394_A909}	TCCTTATACT	GCTGGAGTTT	TAGATGCTTT TCTAGATGCA GGAATAAAAG
msa47199.2{394_H36B}	TCCTTATACT	GCTGGAGTTT	TAGATGCTTT TCTAGATGCA GGAATAAAAG
msa47199.2{394_JM9130013}	TCCTTATACT	GCTGGAGTTT	TAGATGCTTT TCTAGATGCA GGAATAAAAG

Table 77: Comparative Sequences relating toSAG2059

msa47199.2{394_090}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAAATAAAAA
msa47199.2{394_18RS21}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAAATAAAAA
msa47199.2{394_2603}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAAATAAAAA
msa47199.2{394_CJB110}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAAATAAAAA
msa47199.2{394_COH1}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAAATAAAAA
msa47199.2{394_M732}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAAATAAAAA
msa47199.2{394_M781}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAAATAAAAA
msa47199.2{394_1169NT}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAAATAAAAA
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	TAGATGGTAT	CaTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_H36B}	TAGATGGTAT	CaTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_JM9130013}	TAGATGGTAT	CaTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_090}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_18RS21}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_2603}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_CJB110}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_COH1}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_M732}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_M781}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_1169NT}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAAATTTT
Consensus	*****	*-*****	*****	*****	*****
msa47199.2{394_A909}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_H36B}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_JM9130013}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_090}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_18RS21}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_2603}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_CJB110}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_COH1}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_M732}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_M781}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_1169NT}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTTATC
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_H36B}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_JM9130013}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_090}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_18RS21}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_2603}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_CJB110}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_COH1}	CCACCCTgAA	TATATGAGTC	TAAGaTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_M732}	CCACCCTgAA	TATATGAGTC	TAAGaTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_M781}	CCACCCTgAA	TATATGAGTC	TAAGaTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_1169NT}	CCACCCTaAA	TATATGAGTC	TAAGaTCATG	GcTTcGAACA	GGGAATTTTG
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_H36B}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_JM9130013}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_090}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_18RS21}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_2603}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_CJB110}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_COH1}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_M732}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_M781}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_1169NT}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_H36B}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_JM9130013}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_090}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_18RS21}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_2603}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_CJB110}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_COH1}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_M732}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_M781}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_1169NT}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	AGAGATGACA	TCTGGTAAAC	CTGAgTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_H36B}	AGAGATGACA	TCTGGTAAAC	CTGAgTATTT	TAAAATTGAT	AGTGTtTTTG

Table 77: Comparative Sequences relating toSAG2059

msa47199.2{394_JM9130013}	AGAGATGACA	TCTGGTAAAC	CTGAgTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_090}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_18RS21}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_2603}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_CJB110}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_COH1}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_M732}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_M781}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_1169NT}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_H36B}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_JM9130013}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_090}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_18RS21}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_2603}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_CJB110}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_COH1}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_M732}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_M781}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_1169NT}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_H36B}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_JM9130013}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_090}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_18RS21}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_2603}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_CJB110}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_COH1}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_M732}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_M781}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_1169NT}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_H36B}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_JM9130013}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_090}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_18RS21}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_2603}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_CJB110}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_COH1}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_M732}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_M781}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_1169NT}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
Consensus	***-*****	*****	*****	*****	*****
msa47199.2{394_A909}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_H36B}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_JM9130013}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_090}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_18RS21}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_2603}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_CJB110}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_COH1}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_M732}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_M781}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_1169NT}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_H36B}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_JM9130013}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_090}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_18RS21}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_2603}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_CJB110}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_COH1}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_M732}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_M781}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_1169NT}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	cCGGTACCAA	CAGTATAATA	ATAGcCTTGA	AAAGGTCATG	AGCCTTGAAA

Table 77: Comparative Sequences relating to SAG2059

msa47199.2{394_H36B}	cCGGTACCAA	CAGTATAATA	ATAGcCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_JM9130013}	cCGGTACCAA	CAGTATAATA	ATAGcCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_090}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_18RS21}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_2603}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_CJB110}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_COH1}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_M732}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_M781}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_1169NT}	tCGGTACCAA	CAGTATAATA	ATAGcCTTGA	AAAGGTCATG	AGCCTTGAAA
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCaA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_H36B}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCaA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_JM9130013}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCaA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_090}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_18RS21}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_2603}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_CJB110}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_COH1}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_M732}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_M781}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_1169NT}	AAACAGGCGA	TCTATTTGCA	ATTAGgCCgA	GTAAaAGCTT	GGTTATTGtC
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_H36B}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_JM9130013}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_090}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_18RS21}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_2603}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_CJB110}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_COH1}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_M732}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_M781}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_1169NT}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	GAAAgATGCT	AAAAGTGgGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_H36B}	GAAAgATGCT	AAAAGTGgGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_JM9130013}	GAAAgATGCT	AAAAGTGgGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_090}	GAAAgATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_18RS21}	GAAAgATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_2603}	GAAAgATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_CJB110}	GAAAgATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_COH1}	GAAAtATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_M732}	GAAAtATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_M781}	GAAAtATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_1169NT}	GAAAgATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
Consensus	*****	*****	*****	*****	*****

SEQ ID NO. 7712

STRAIN 2603 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERLRY
 NKYLKSHPKYMSLRSLRWTGNFVNKDFTYEYVPMKLDVDFDEAFKSSIDFYVATEMTS
 GKPEYFKIDSVEQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IIVMTRLPNYQKKPSSGRLYKTLRYKYPNFVKTASNRYQQYNNLSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPKLDSIYQLGMKDAKSMPELNSYLMK

SEQ ID NO. 7713

STRAIN 090 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERLRY
 NKYLKSHPKYMSLRSLRWTGNFVNKDFTYEYVPMKLDVDFDEAFKSSIDFYVATEMTS
 GKPEYFKIDSVEQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IIVMTRLPNYQKKPSSGRLYKTLRYKYPNFVKTASNRYQQYNNLSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPKLDSIYQLGMKDAKSMPELNSYLMK

SEQ ID NO. 7714

STRAIN A909 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKVDGIIISVSAGALFGVNFVSRQRERLRY
 NKYLKSHPKYMSLRSLRWTGNFVNKDFTYEYVPMKLDVDFDEAFKSSIDFYAVATEMTS
 GKPEYFKIDSVEQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IIVMTRLPNYQKKPSSGRLYKTLRYKYPNFVKTASNRYQQYNNLSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPKLDSIYQLGMKDAKSMPELNSYLMK

SEQ ID NO. 7715

STRAIN H36B frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKVDGIIISVSAGALFGVNFVSRQRERLRY
 NKYLKSHPKYMSLRSLRWTGNFVNKDFTYEYVPMKLDVDFDEAFKSSIDFYAVATEMTS

Table 77: Comparative Sequences relating to SAG2059

GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKASNRYQQYNNSEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7716

STRAIN 18RS21 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERARLY
 NKCYLSHPKYMMSLRSLWRTGNFVNKDFTYEVPKLDVDFDEAFKKSSIDFYVVAEMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKASNRYQQYNNSEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7717

STRAIN M732 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERARLY
 NKCYLSHPKYMMSLRSLWRTGNFVNKDFTYEVPKLDVDFDEAFKKSSIDFYVVAEMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKASNRYQQYNNSEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7718

STRAIN COH1 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERARLY
 NKCYLSHPKYMMSLRSLWRTGNFVNKDFTYEVPKLDVDFDEAFKKSSIDFYVVAEMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKASNRYQQYNNSEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7719

STRAIN M781 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERARLY
 NKCYLSHPKYMMSLRSLWRTGNFVNKDFTYEVPKLDVDFDEAFKKSSIDFYVVAEMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKASNRYQQYNNSEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7720

STRAIN CJB110 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERARLY
 NKCYLSHPKYMMSLRSLWRTGNFVNKDFTYEVPKLDVDFDEAFKKSSIDFYVVAEMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKASNRYQQYNNSEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7721

STRAIN JM9130013 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKVDGIISVSAGALFGVNFVSRQRERARLY
 NKCYLSHPKYMMSLRSLWRTGNFVNKDFTYEVPKLDVDFDEAFKKSSIDFYVVAEMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKASNRYQQYNNSEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7722

STRAIN 1169NT frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERARLY
 NKCYLSHPKYMMSLRSLWRTGNFVNKDFTYEVPKLDVDFDEAFKKSSIDFYVVAEMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKASNRYQQYNNSEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

	1				50
msa47322.2{394_A909}	PMLSVGLVLE	GGGMRGLYTA	GVLDAFLDAG	IKVDGIISVS	AGALFGVNFV
msa47322.2{394_H36B}	PMLSVGLVLE	GGGMRGLYTA	GVLDAFLDAG	IKVDGIISVS	AGALFGVNFV
msa47322.2{394_JM9130013}	PMLSVGLVLE	GGGMRGLYTA	GVLDAFLDAG	IKVDGIISVS	AGALFGVNFV
msa47322.2{394_090}	PMLSVGLVLE	GGGMRGLYTA	GVLDAFLDAG	IKIDGIVSVS	AGALFGVNFV
msa47322.2{394_1169NT}	PMLSVGLVLE	GGGMRGLYTA	GVLDAFLDAG	IKIDGIVSVS	AGALFGVNFV
msa47322.2{394_18RS21}	PMLSVGLVLE	GGGMRGLYTA	GVLDAFLDAG	IKIDGIVSVS	AGALFGVNFV
msa47322.2{394_2603}	PMLSVGLVLE	GGGMRGLYTA	GVLDAFLDAG	IKIDGIVSVS	AGALFGVNFV
msa47322.2{394_CJB110}	PMLSVGLVLE	GGGMRGLYTA	GVLDAFLDAG	IKIDGIVSVS	AGALFGVNFV
msa47322.2{394_COH1}	PMLSVGLVLE	GGGMRGLYTA	GVLDAFLDAG	IKIDGIVSVS	AGALFGVNFV
msa47322.2{394_M732}	PMLSVGLVLE	GGGMRGLYTA	GVLDAFLDAG	IKIDGIVSVS	AGALFGVNFV
msa47322.2{394_M781}	PMLSVGLVLE	GGGMRGLYTA	GVLDAFLDAG	IKIDGIVSVS	AGALFGVNFV
Consensus	*****	*****	*****	**--*-***	*****
	51				100
msa47322.2{394_A909}	SRQRERARLY	NKKYLSHPKY	MSLRSLWRTG	NFVNKDFTYY	EVPMKLDVFD
msa47322.2{394_H36B}	SRQRERARLY	NKKYLSHPKY	MSLRSLWRTG	NFVNKDFTYY	EVPMKLDVFD
msa47322.2{394_JM9130013}	SRQRERARLY	NKKYLSHPKY	MSLRSLWRTG	NFVNKDFTYY	EVPMKLDVFD
msa47322.2{394_090}	SRQRERARLY	NKKYLSHPKY	MSLRSLWRTG	NFVNKDFTYY	EVPMKLDVFD
msa47322.2{394_1169NT}	SRQRERARLY	NKKYLSHPKY	MSLRSLWRTG	NFVNKDFTYY	EVPMKLDVFD
msa47322.2{394_18RS21}	SRQRERARLY	NKKYLSHPKY	MSLRSLWRTG	NFVNKDFTYY	EVPMKLDVFD

Table 77: Comparative Sequences relating toSAG2059

msa47322.2{394_2603}	SRQRERALRY	NKKYLShPKY	MSLRswfRTG	NFVNkdFTYY	EVPMKLDVFD
msa47322.2{394_CJB110}	SRQRERALRY	NKKYLShPKY	MSLRswfRTG	NFVNkdFTYY	EVPMKLDVFD
msa47322.2{394_COH1}	SRQRERALRY	NKKYLShPeY	MSLRswlRTG	NFVNkdFTYY	EVPMKLDVFD
msa47322.2{394_M732}	SRQRERALRY	NKKYLShPeY	MSLRswlRTG	NFVNkdFTYY	EVPMKLDVFD
msa47322.2{394_M781}	SRQRERALRY	NKKYLShPeY	MSLRswlRTG	NFVNkdFTYY	EVPMKLDVFD
Consensus	*****	*****-*	*****-***	*****	*****
msa47322.2{394_A909}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_H36B}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_JM9130013}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_090}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_1169NT}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_18RS21}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_2603}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_CJB110}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_COH1}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_M732}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_M781}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
Consensus	*****	**_*****	*****	*****	*****
msa47322.2{394_A909}	VvWQGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_H36B}	VvWQGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_JM9130013}	VvWQGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_090}	VdWQGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_1169NT}	VdWQGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_18RS21}	VdWQGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_2603}	VdWQGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_CJB110}	VdWQGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_COH1}	VdWQGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_M732}	VdWQGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_M781}	VdWQGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
Consensus	*_******	*****	*****	*****	*****
msa47322.2{394_A909}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIGr
msa47322.2{394_H36B}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIGr
msa47322.2{394_JM9130013}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIGr
msa47322.2{394_090}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIGr
msa47322.2{394_1169NT}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIGr
msa47322.2{394_18RS21}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIGr
msa47322.2{394_2603}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIGr
msa47322.2{394_CJB110}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIGr
msa47322.2{394_COH1}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIGr
msa47322.2{394_M732}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIGr
msa47322.2{394_M781}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIGr
Consensus	*****	*****	*****	*****	*****_*
msa47322.2{394_A909}	LEKNPDKLDS	IYQLGMKdAK	SgMPELNSYL	MK	
msa47322.2{394_H36B}	LEKNPDKLDS	IYQLGMKdAK	SgMPELNSYL	MK	
msa47322.2{394_JM9130013}	LEKNPDKLDS	IYQLGMKdAK	SgMPELNSYL	MK	
msa47322.2{394_090}	LEKNPDKLDS	IYQLGMKdAK	SvMPELNSYL	MK	
msa47322.2{394_1169NT}	LEKNPDKLDS	IYQLGMKdAK	SvMPELNSYL	MK	
msa47322.2{394_18RS21}	LEKNPDKLDS	IYQLGMKdAK	SvMPELNSYL	MK	
msa47322.2{394_2603}	LEKNPDKLDS	IYQLGMKdAK	SvMPELNSYL	MK	
msa47322.2{394_CJB110}	LEKNPDKLDS	IYQLGMKdAK	SvMPELNSYL	MK	
msa47322.2{394_COH1}	LEKNPDKLDS	IYQLGMKyAK	SvMPELNSYL	MK	
msa47322.2{394_M732}	LEKNPDKLDS	IYQLGMKyAK	SvMPELNSYL	MK	
msa47322.2{394_M781}	LEKNPDKLDS	IYQLGMKyAK	SvMPELNSYL	MK	
Consensus	*****	*****_*	*_******	**	

Table 78: Comparative Sequences relating to SAG1016

SEQ ID NO. 7801

STRAIN 2603

ATGAAAGTTTGTAGTTGATGATGAACCAAGTTGCACGTAACGAATTAATTTACCTTCTT
 AATAAGATGATTTCTAACCTCGTTATAGCAGAGGCGCATGATATGGCTACTGCATTAGCT
 ATTTTACTTAGAGAACTTTTGTAGTAGCACTGTTAGATATCCATCTCAGAGATGATTCT
 GGGTTGCAATTAGCAGAGTATATCAATAAAATGCCAAACCACCATTATTGATATTTGCG
 ACTGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCATGATGCGCGTGATTATTTGTTA
 AAACCCCTATGATTTTGTATAGGCTAAAGCAAGCTATGGATAGAGTAAAGGAGCGCTAAGT
 ACATCTACAATTTATAGAGAGCGTAACCTCCGGTCTCTCTTCAAGCAACAGTATCCATTG
 ACAGTAGAAGATCGAATCTATCTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATG
 CAAGGAAAACTGATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACAA
 CAATGGCAAGATAAATACCATCATCTCAATTTGTACGGGTACATCGCTCTTACATTGTG
 AACATTAATGCTATTAAACGATTGAACCTTGGTTTAAACCAACACTTCAGTTACACCTT
 TGTATAAAATAACAGTTCCTGTTAGCAGAGCAATGTAAACCCCTAAACAAATGTTA
 GGCATATCTACC

SEQ ID NO. 7802

STRAIN 090

AAAGTTTGTAGTTGATGATGAACCAAGTTGCACGTAA
 CGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAG
 AGGCGCATGATATGGCTACTGCACTAGCTATTTTACTTAGAGAACTTTT
 GATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATT
 AGCAGAGTATATCAATAAAATGCCAAACCACCATTATTGATATTTGCGA
 CTGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCATGATGCGCGTGAT
 TATTTGTAAACCCCTATGATTTTGTATAGGCTAAAGCAAGCTATGGATAG
 AGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACCTCCG
 GTCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTAT
 CTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAACT
 GATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACAAC
 AATGGCAAGATAAATACCATCATCTCAATTTGTACGGGTACATCGCTCT
 TACATTGTGAACATTAATGCTATTAAACGATTGAACCTTGGTTTAAACCA
 AACCTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAGAG
 CAAATGTAAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7803

STRAIN A909

AAAGTTTGTAGTTGATGATGAACCAAGTTGCACGTAA
 GAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAG
 GCGCATGATATGGCTACTGCACTAGCTATTTTACTTAGAGAACTTTT
 ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATTA
 GCAGAGTATATCAATAAAATGCCAAACCACCATTATTGATATTCGCGAC
 TGCTTATGATCAATATGCTATTCAAGCTTTTGAGCATGATGCGCGTGATT
 ATTTGTTAAACCCCTATGAGTTTGTATAGGCTAAAGCAAGCTATGGATAGA
 GTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACCTCCGG
 CCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTATC
 TGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAACTG
 ATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACAACA
 ATGGCAAGATAAATACCATCATCTCAATTTGTACGGGTGACCGCTCTT
 ACATTGTGAATATTAAATGCTATTAAACGATTGAACCTTGGTTTAAACCA
 ACACCTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAGAG
 AAATGTAAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7804

STRAIN H36B

AAAGTTTGTAGTTGATGATGAACCAAGTTGCACGT
 AACGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGC
 AGAGGCGCATGATATGGCTACTGCACTAGCTATTTTACTTAGAGAACTT
 TTGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAA
 TTAGCAGAGTATATCAATAAAATGCCAAACCACCATTATTGATATTCGC
 GACTGCTTATGATCAATATGCTATTCAAGCTTTTGAGCATGATGCGCGTG
 ATTATTTGTTAAACCCCTATGAGTTTGTATAGGCTAAAGCAAGCTATGGAT
 AGAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACCTC
 CGGCCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCT
 ATCTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAA
 CTGATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACA
 ACAATGGCAAGATAAATACCATCATCTCAATTTGTACGGGTGACCGCT
 CTTACATTGTGAATATTAAATGCTATTAAACGATTGAACCTTGGTTTAAAC
 CAAACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAG
 AGCAATGTAAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7805

STRAIN 18RS21

AAAGTTTGTAGTTGATGATGAACCAAGTTGCACGTAA
 GAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAG
 GCGCATGATATGGCTACTGCACTAGCTATTTTACTTAGAGAACTTTT
 ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATTA
 GCAGAGTATATCAATAAAATGCCAAACCACCATTATTGATATTTGCGAC
 TGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCATGATGCGCGTGATT
 ATTTGTTAAACCCCTATGATTTTGTATAGGCTAAAGCAAGCTATGGATAGA
 GTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACCTCCGG
 TCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTATC
 TGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAACTG

Table 78: Comparative Sequences relating to SAG1016

ATTATACAAACACCTGATAAAATTTATGAAATTTGATGGCTCTCTACAACA
 ATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTCTT
 ACATTTGTGAACATTAAATGCTATTAAAAACGATTGAACCTTGGTTTAAACCAA
 ACATTTGAGTTACACCTTTGTAATAAAATAACAGTTCTCTGTTAGCAGAGC
 AAATGTAAACCCCTAAACCAAATGTTAGGCATATCTACC

SEQ ID NO. 7806

STRAIN M732

AAAGTTTTAGTAGTTGATGATGAACCAAGTT
 GCACGTAACGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGT
 TATAGCAGAGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAG
 AAATTTTGTAGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGG
 TTGCAATTAGCAGAGTATATCAATAAAATGCCAAACCAACCAATTATTGAT
 ATTCGCGCACTGCTTATGATCAATATGCTATTCAAGGCTTTTGAGCAGGATG
 CGCGTGATTATTTGTTAAACCCCTATGAGTTTGTAGGTTAAAGCAAGCT
 ATGGATAGAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGT
 AGCTTCCGGTCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATC
 GAATCTATCTGGTGTGCGCGGATGATATCCCTTTTGATTGAAGCTATGCAA
 GGAAAACTGATTATACAAACACCTGATAAAAAATTATGAAATTTGATGGCTC
 TCTACAACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTAC
 ATCGCTCTTACATTGTGAATATTAATGCTATTAAACGATTGAACCTTGG
 TTTAACCAACACCTTCAGTTACACCTTTGTAATAAAATAACAGTTCTCTGT
 TAGCAGAGCAATGTAAACCCCTAAACCAAATGTTAGGCATATCTACC

SEQ ID NO. 7807

STRAIN COH1

AAAGTTTTAGTAGTTGATGATGAACCAAGTTGCACGTA
 ACCGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCA
 GAGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAGAACTTT
 TGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAAT
 TAGCAGAGTATATCAATAAAATGCCAAACCAACCAATTATTGATATTCGCG
 ACTGCTTATGATCAATATGCTATTCAAGGCTTTTGAGCAGGATGCGCGTGA
 TTATTTGTTAAACCCCTATGAGTTGTAGGTTAAAGCAAGCTATGGATA
 GAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAGCTTCC
 GGTCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTA
 TCTGGTGTGCGCGGATGATATCCCTTTTGATTGAAGCTATGCAAGGAAAC
 TGATTATACAAACACCTGATAAAAAATTATGAAATTTGATGGCTCTCTACAA
 CAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTC
 TTACATTGTGAATATTAATGCTATTAAACGATTGAACCTTGGTTTAAACC
 AAACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCTCTGTTAGCAGA
 GCAATGTAAACCCCTAAACCAAATGTTAGGCATATCTACC

SEQ ID NO. 7808

STRAIN M781

AAAGTTTTAGTAGTTGATGATGAACCAAGTTGCACGTAAC
 GAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAGA
 GGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAGAACTTTTG
 ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATTA
 GCAGAGTATATCAATAAAATGCCAAACCAACCAATTATTGATATTCGCGAC
 TGCTTATGATCAATATGCTATTCAAGGCTTTTGAGCAGGATGCGCGTGATT
 ATTTGTTAAAAACCCCTATGAGTTTGATAGGTTAAAGCAAGCTATGGATAGA
 GTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAGCTTCCGG
 TCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTATC
 TGGTGTGCGCGGATGATATCCCTTTTGATTGAAGCTATGCAAGGAAACCTG
 ATTATACAAACACCTGATAAAAAATTATGAAATTTGATGGCTCTCTACAACA
 ATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTCTT
 ACATTGTGAATATTAATGCTATTAAACGATTGAACCTTGGTTTAAACCAA
 ACACCTTCAGTTACACCTTTGTAATAAAATAACAGTTCTCTGTTAGCAGAGC
 AAATGTAAACCCCTAAACCAAATGTTAGGCATATCTACC

SEQ ID NO. 7809

STRAIN CJB110

CTTAATAAGTATGATTCTAACCTCGTTATAGCAGAGGCGCATGATATGGC
 TACTGCATTAGCTATTTTACTTAGAGAACTTTTGATGTAGCACTGTTAG
 ATATCCATCTCAGAGATGATTCTGGGTTGCAATTAGCAGAGTATATCAAT
 AAAATGCCAAACCAACCAATTATTGATATTCGCGACTGCTTATGATCAATA
 TGCTATTCAAGCTTTTGAGCATGATGCGCGTGATTATTTGTTAAACCCCT
 ATGAGTTTGATAGGCTAAAGCAAGTATGGATAGAGTAAAGGAGCGCTA
 AGTACATCTACAATTATAGAGAGCGTAACCTTCGGCCCTCTCTTCAAGCA
 ACAGTATCCATTGACAGTAGAAGATnGAATCTATCTGGTGTGCGCGGATG
 ATATCCTTTTGATTGAAGCTATGCAAGGAAACCTGATTATACAAACACCT
 GATAAAAAATTATGAAATTTGATGGCTCTCTACAACAATGGCAAGATAAACT
 ACCATCATCTCAATTTGTACGGGTGCAACCGCTCTTACATTGTGAATATTA
 ATGCTATTAACGAGATTGAACCTTGGTTTAAACCAACACTTCAGTTACAC
 CTTTGTAAATAAAATAACAGTTCTCTGTTAGCAGAGCAATGTAAACCCCT
 AAAACAAATGTTAGG

SEQ ID NO. 7810

STRAIN 1169NT

AAAGTTTTAGTAGTTGATGATGAACCAAG
 TTGCACGTAACGAATTAATTTATCTTCTTAATAAGTATGATTCTAACCTC
 GTTATAGCAGAGGCGCATGATATAGCTACTGCATTAGCTATTTTACTTAG

Table 78: Comparative Sequences relating to SAG1016

AGAAACCTTTTGTAGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTG
GGTTGCAATTAGCAGAGTATATCAATAAAATGCCCAAACCACTATTATG
ATATTCCGCACTGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCATGA
TGCCTGTGATTATTTGTTAAACCCCTATGAGTTTGATAGGCTAAAGCAAG
CTATGGATAGAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGC
GTAACCTCCGGCCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGA
TCGAATCTATCTGGTGTGCGCGGATGATATCCCTTTTGATTGAAGCTATGC
AAGGAAAACGTATTATACAAACACCTGATAAAAATTATGAAATTGATGGC
TCTCTACAACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGT
GCACCGCTCTTACATTTGTGAATATTAATGCTATTAAACGATTGAACCTT
GGTTTAAACCAACACCTTCAGTTACACCTTTGTAATAAAATAACAGTTCCCT
GTTAGCAGAGCAAATGTAAACCCCTAAACAAATGTTAGGCATATCTAC
C

SEQ ID NO. 7811

STRAIN JM9130013

AAAGTTTTAGTAGTTGATGATGAACCACT

TGCACGTAAACGAATTAATTACCTTCTTAATAAGTATGATTCTAACCTCG
TTATAGCAGAGGCGCATGATATGGCTACTGCAATTAGCTATTTTACTTAGA
GAAACTTTTGTAGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGG
GTTGCAATTAGCAGAGTATATCAATAAAATGCCCAAACCACTATTATGTA
TATTCCGCACTGCTTATGATCAATATGCTATTCAAGCTTTTGAGCATGAT
GCGCGTGATTATTTGTTAAACCCCTATGAGTTTGATAGGCTAAAGCAAGC
TATGGATAGAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCG
TAACCTTCGCGCCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGAT
CGAATCTATCTGGTGTGCGCGGATGATATCCCTTTTGATTGAAGCTATGCA
AGGAAAACCTGATTATACAAACACCTGATAAAAATTATGAAATTGATGGCT
CTCTACACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTG
CACCGCTCTTACATTTGTGAATATTAATGCTATTAAACGATTGAACCTTG
GTTTAAACCAACACCTTCAGTTACACCTTTGTAATAAAATAACAGTTCCCTG
TTAGCAGAGCAAATGTAAACCCCTAAACAAATGTTAGGCATATCTACC

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa141507.2{*} April 10, 2003 06:36 ..

	1		50
msa141507.2{399_A909}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_CJB110}	-----	-----	-----
msa141507.2{399_H36B}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_JM9130013}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_1169NT}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_090}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_18RS21}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_2603}	atgaaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_COH1}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_M732}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_M781}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
Consensus	*****	-----	-----
	51		100
msa141507.2{399_A909}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_CJB110}	-----CTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_H36B}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_JM9130013}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_1169NT}	ttatcttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_090}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_18RS21}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_2603}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_COH1}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_M732}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_M781}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
Consensus	-----	*****	*****
	101		150
msa141507.2{399_A909}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_CJB110}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_H36B}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_JM9130013}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_1169NT}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_090}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_18RS21}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_2603}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_COH1}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_M732}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_M781}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
Consensus	*****	*****	*****
	151		200
msa141507.2{399_A909}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT GGGTTGCAAT TAGCAGAGTA
msa141507.2{399_CJB110}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT GGGTTGCAAT TAGCAGAGTA
msa141507.2{399_H36B}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT GGGTTGCAAT TAGCAGAGTA
msa141507.2{399_JM9130013}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT GGGTTGCAAT TAGCAGAGTA
msa141507.2{399_1169NT}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT GGGTTGCAAT TAGCAGAGTA

Table 78: Comparative Sequences relating to SAG1016

msa141507.2{399_090}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_18RS21}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_2603}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_COH1}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_M732}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_M781}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
Consensus	*****	*****	*****	*****	*****
msa141507.2{399_A909}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_CJB110}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_H36B}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_JM9130013}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_1169NT}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_090}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_18RS21}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_2603}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_COH1}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_M732}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_M781}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
Consensus	*****	*****	*****	*****-***	*****
msa141507.2{399_A909}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTGA
msa141507.2{399_CJB110}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTGA
msa141507.2{399_H36B}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTGA
msa141507.2{399_JM9130013}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTGA
msa141507.2{399_1169NT}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTGA
msa141507.2{399_090}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTGA
msa141507.2{399_18RS21}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTGA
msa141507.2{399_2603}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTGA
msa141507.2{399_COH1}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTGA
msa141507.2{399_M732}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTGA
msa141507.2{399_M781}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTGA
Consensus	*****	*****-***	*****-*	*****	*****
msa141507.2{399_A909}	AAACCCCTATG	AgTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_CJB110}	AAACCCCTATG	AgTTTGATAG	GcTAAAGCAA	GnTATGGATA	GAGTAAAGG
msa141507.2{399_H36B}	AAACCCCTATG	AgTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_JM9130013}	AAACCCCTATG	AgTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_1169NT}	AAACCCCTATG	AgTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_090}	AAACCCCTATG	AtTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_18RS21}	AAACCCCTATG	AtTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_2603}	AAACCCCTATG	AtTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_COH1}	AAACCCCTATG	AgTTTGATAG	GtTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_M732}	AAACCCCTATG	AgTTTGATAG	GtTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_M781}	AAACCCCTATG	AgTTTGATAG	GtTAAAGCAA	GcTATGGATA	GAGTAAAGG
Consensus	*****	*-*****	*-*****	*-*****	*****
msa141507.2{399_A909}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_CJB110}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_H36B}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_JM9130013}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_1169NT}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_090}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_18RS21}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_2603}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_COH1}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_M732}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_M781}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
Consensus	*****	*****	*****	*****	*****
msa141507.2{399_A909}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_CJB110}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATnGAATCTA	TCTGGTGTCTG
msa141507.2{399_H36B}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_JM9130013}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_1169NT}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_090}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_18RS21}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_2603}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_COH1}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_M732}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_M781}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
Consensus	*****	*****	*****	**-*****	*****
msa141507.2{399_A909}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_CJB110}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_H36B}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_JM9130013}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA

Table 78: Comparative Sequences relating to SAG1016

msa141507.2{399_1169NT}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_090}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_18RS21}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_2603}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_COH1}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_M732}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_M781}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
Consensus	*****	*****	*****	*****	*****
msa141507.2{399_A909}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_CJB110}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_H36B}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_JM9130013}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_1169NT}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_090}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_18RS21}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_2603}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_COH1}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_M732}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_M781}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
Consensus	*****	*****	*****	*****	*****
msa141507.2{399_A909}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCAcCGCTC	TTACATTGTG
msa141507.2{399_CJB110}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCAcCGCTC	TTACATTGTG
msa141507.2{399_H36B}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCAcCGCTC	TTACATTGTG
msa141507.2{399_JM9130013}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCAcCGCTC	TTACATTGTG
msa141507.2{399_1169NT}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCAcCGCTC	TTACATTGTG
msa141507.2{399_090}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_18RS21}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_2603}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_COH1}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_M732}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_M781}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
Consensus	*****	*****	*****	*_...*****	*****
msa141507.2{399_A909}	AAtATTAATG	CTATTAAAAAC	GATTGAACCT	TGGTTTAAAC	AAACACTTCA
msa141507.2{399_CJB110}	AAtATTAATG	CTATTAAAAAC	GATTGAACCT	TGGTTTAAAC	AAACACTTCA
msa141507.2{399_H36B}	AAtATTAATG	CTATTAAAAAC	GATTGAACCT	TGGTTTAAAC	AAACACTTCA
msa141507.2{399_JM9130013}	AAtATTAATG	CTATTAAAAAC	GATTGAACCT	TGGTTTAAAC	AAACACTTCA
msa141507.2{399_1169NT}	AAtATTAATG	CTATTAAAAAC	GATTGAACCT	TGGTTTAAAC	AAACACTTCA
msa141507.2{399_090}	AAtATTAATG	CTATTAAAAAC	GATTGAACCT	TGGTTTAAAC	AAACACTTCA
msa141507.2{399_18RS21}	AAtATTAATG	CTATTAAAAAC	GATTGAACCT	TGGTTTAAAC	AAACACTTCA
msa141507.2{399_2603}	AAtATTAATG	CTATTAAAAAC	GATTGAACCT	TGGTTTAAAC	AAACACTTCA
msa141507.2{399_COH1}	AAtATTAATG	CTATTAAAAAC	GATTGAACCT	TGGTTTAAAC	AAACACTTCA
msa141507.2{399_M732}	AAtATTAATG	CTATTAAAAAC	GATTGAACCT	TGGTTTAAAC	AAACACTTCA
msa141507.2{399_M781}	AAtATTAATG	CTATTAAAAAC	GATTGAACCT	TGGTTTAAAC	AAACACTTCA
Consensus	**_*****	*****	*****	*****	*****
msa141507.2{399_A909}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_CJB110}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_H36B}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_JM9130013}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_1169NT}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_090}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_18RS21}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_2603}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_COH1}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_M732}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_M781}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
Consensus	*****	*****	*****	*****	*****
msa141507.2{399_A909}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_CJB110}	AACCCCTAAA	ACAAATGTTA	GG-----	--	
msa141507.2{399_H36B}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_JM9130013}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_1169NT}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_090}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_18RS21}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_2603}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_COH1}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_M732}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_M781}	AACCCCTAAA	ACAAATGTIA	GGcatatcta	cc	
Consensus	*****	*****	***-----	--	

SEQ ID NO. 7812

STRAIN 2603 frame: 1

KVLVVDDEBPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
 LQLAEYINKMPKPLLIIFATAYDQYAIQAFEHDDARDYLLKPYDFDRLKQAMDRVKGALST

Table 78: Comparative Sequences relating to SAG1016

STIIESVTSGLPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7813

STRAIN 090 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGLPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7814

STRAIN A909 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGLPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7815

STRAIN H36B frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGLPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7816

STRAIN 18RS21 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGLPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7817

STRAIN M732 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGLPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7818

STRAIN COH1 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGLPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7819

STRAIN M781 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGLPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7820

STRAIN CJB110 frame: 1

LNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG LQLAEYINKMPKPPLLI F
ATAYDQYAI QAFEHDARDYLLKPYEFDRLKQXMDRVKGALSTSTIIESVTSGLPLFKQQYP
LTVEDXIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQWQDKLPSSQFVRVHRSYI
VNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQML

SEQ ID NO. 7821

STRAIN 1169NT frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDIATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGLPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7822

STRAIN JM9130013 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGLPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

Table 78: Comparative Sequences relating to SAG1016

PRETTY of: /biotmp/msa141801.2{*} April 10, 2003 06:38 ..

	1				50
msa141801.2{399_COH1}	kvlvvdddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_M732}	kvlvvdddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_M781}	kvlvvdddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_090}	kvlvvdddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_18RS21}	kvlvvdddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_2603}	kvlvvdddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_A909}	kvlvvdddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_H36B}	kvlvvdddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_JM9130013}	kvlvvdddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_1169NT}	kvlvvdddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_CJB110}	-----LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL	-----
Consensus	-----	*****	*****	*****	*****
	51				100
msa141801.2{399_COH1}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EqDARDYLLK
msa141801.2{399_M732}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EqDARDYLLK
msa141801.2{399_M781}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EqDARDYLLK
msa141801.2{399_090}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EhDARDYLLK
msa141801.2{399_18RS21}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EhDARDYLLK
msa141801.2{399_2603}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EhDARDYLLK
msa141801.2{399_A909}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EhDARDYLLK
msa141801.2{399_H36B}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EhDARDYLLK
msa141801.2{399_JM9130013}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EhDARDYLLK
msa141801.2{399_1169NT}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EhDARDYLLK
msa141801.2{399_CJB110}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EhDARDYLLK
Consensus	*****	*****	*****	*****	*****
	101				150
msa141801.2{399_COH1}	PYeFDRLKQa	MDRVKGALST	STIIESVaSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_M732}	PYeFDRLKQa	MDRVKGALST	STIIESVaSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_M781}	PYeFDRLKQa	MDRVKGALST	STIIESVaSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_090}	PYdFDRLKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_18RS21}	PYdFDRLKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_2603}	PYdFDRLKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_A909}	PYeFDRLKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_H36B}	PYeFDRLKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_JM9130013}	PYeFDRLKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_1169NT}	PYeFDRLKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_CJB110}	PYeFDRLKQx	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDxIYLVSA
Consensus	**-----	*****	*****	*****	**-----
	151				200
msa141801.2{399_COH1}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_M732}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_M781}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_090}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_18RS21}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_2603}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_A909}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_H36B}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_JM9130013}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_1169NT}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_CJB110}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
Consensus	*****	*****	*****	*****	*****
	201				243
msa141801.2{399_COH1}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_M732}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_M781}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_090}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_18RS21}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_2603}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_A909}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_H36B}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_JM9130013}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_1169NT}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_CJB110}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQML-	---
Consensus	*****	*****	*****	*****	---

Table 79: Comparative Sequences relating to SAG2150

SEQ ID NO. 7901

STRAIN 2603

ATGGGAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCCGGCACTCCTTTTGAAGGG
CGTGCCCTTTTGGACGTCAATCTGAAAATTGAAGATGCTTCTATACCGCGTTTCATTGGG
CACACAGGTTCTGAAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCTTACA
AAAGGTGAGGTAATTGTCGATGATTTTCTATTAAAGCAGGGGACAAGAACAAGAAATC
AAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCAGAAAGTCAGCTTTTGA
GAGACAGTTTAAAGGATGTTGCTTTTGGACCACAAAATTTTGGTATTCTCAGATTGAA
GCTGAAAGGCTGGCTGAAGAAAATTAAGGTTAGTTGGTATCAGTGAGGATTATTTCGAT
AAAAATCCATTTGAACCTTTCTGGAGGGCAGATGAGGCGGGTGTCTATAGCTGGTATTTTA
GCGATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATCCTAAGGGA
AGAAAAGAATTAAATGACTCTTTTAAAAATCTTCATAAAAAAGGAATGACTATCGTCTTA
GTGACTCACTTAATGGACGATGTAGCGGATTATGCTGACTATGTGTATGTTTGAAGCA
GGGAAAGTAACCTTATCAGGACAACCAAAACAGATTTTCAAGAAGTAGAATTTTAGAA
AGTAACAATTAGGAGTTCCCAAAATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGA
TTAAATTTACCTAGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTAAAGCATGGA

SEQ ID NO. 7902

STRAIN 090

GGAAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCC
GGCACTCCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATCTGAAAATTGA
AGATGCTTCTATACCGCGTTTCATTGGGCACACAGGTTCTGGAAAATCAA
CTATTATGCACTTTTGAATGGTTTACATATTCTTACAAAAGGTGAGGTA
ATTGTGATGATTTTCTATTAAAGCAGGGGACAAGAACAAGAAATCAA
ATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCAGAAAGTCAGC
TTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACCACAAAATTTT
GGTATTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAAAATTAAGGTT
AGTTGGTATCAGTGAGGATTATTCGATAAAAATCCATTGAACTTTCTG
GAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGCGATGGAACCC
AAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATCCTAAGGGGAAG
AAAAGAATTAAATGACTCTTTTAAAAATCTTCATAAAAAAGGAATGACTA
TCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTATGCTGACTAT
GTGTATGTTTGAAGCAGGGGAAAGTAACCTTATCAGGACAACCAAAACA
GATTTTCAAGAAGTAGAATCTTTAGAAAAGTAACAATTAGGAGTTCCCA
AAATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGATTAAATTTACCT
AGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTAAAGCATGGA

SEQ ID NO. 7903

STRAIN A909

GGAAATTGAATTTAAAAATGTAAGTTATACCTATCAA
GCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATCTGAAAAT
TGAAGATGCTTCTATACCGCGTTTCATTGGGCACACAGGTTCTGGAAAAT
CAACTATTATGCACTTTTGAATGGTTTACATATTCTTACAAAAGGTGAG
GTAATTGTCGATGATTTTCTATTAAAGCAGGGGACAAGAACAAGAAAT
CAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCAGAAAGTC
AGCTTTTGAAGAGACAGTTTAAAGATGTTGCTTTTGGACCACAAAAT
TTTGGTATTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAAAATTAAG
GTTAGTTGGTATCAGTGAGGATTATTCGATAAAAATCCATTGAACTTT
CTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGCGATGGA
CCCAAAGTACTAGTACTAGATGAGCCAACAGCTGGACTTGATCCTAAGGG
AAGAAAAGAATTAAATGACTCTTTTAAAAATCTTCATAAAAAAGGAATGA
CTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTATGCTGAC
TATGTGTATGTTTGAAGCAGGGGAAAGTAACCTTATCAGGACAACCAAA
GCAGATTTTCAAGAAGTAGAATCTTTAGAAAAGTAACAATTAGGAGTTT
CCAAAATCACCAGTTTGTCTCAAAGGCTATCTCATAAGGGATTAAATTTA
CCTAGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTAAAGCATGG
A

SEQ ID NO. 7904

STRAIN H36B

GGAAATTGAATTTAAAAATGTAAGTTATAC
CTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATC
TGAAAATTGAAGATGCTTCTATACCGCGTTTCATTGGGCACACAGGTTCT
GGAAAATCACTATTATGCACTTTTGAATGGTTTACATATTCTTACAAA
AGGTGAGGTAATTGTCGATGATTTTCTATTAAAGCAGGGGACAAGAACA
AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCA
GAAAGTCAGCTTTTGAAGAGACAGTTTAAAGATGTTGCTTTTGGACC
ACAAAATTTGGTATTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
AATTAAAGGTTAGTTGGTATCAGTGAGGATTATTCGATAAAAATCCATT
GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGC
GATGGAACCCAAAGTACTAGTACTAGATGAGCCAACAGCTGGACTTGATC
CTAAGGGAAGAAAAGAATTAAATGACTCTTTTAAAAATCTTCATAAAAA
GGAAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATT
TGCTGACTATGTGTATGTTTGAAGCAGGGGAAAGTAACCTTATCAGGAC
AACCAAGCAGATTTTCAAGAAGTAGAATCTTTAGAAAAGTAACAATTAG
GGAGTTCCCAAAATCACCAGTTTGTCTCAAAGGCTATCTCATAAGGGATT
AAATTTACCTAGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATT
AGCATGGA

SEQ ID NO. 7905

STRAIN 18RS21

GGAAATTGAATTTAAAAATGTAAGTTATAC
CTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATC

Table 79: Comparative Sequences relating to SAG2150

TGAAAATTGAAGATGCTTCCTATACCGCGTTCATTGGGCACACAGGTTCT
 GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCTACAAA
 AGGTGAGGTAATTTGTCGATGATTTTCTATTAAAGCAGGGGACAAGAACA
 AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTCAATTTCCA
 GAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACC
 ACAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAAGTTAGTTGGTATCAGTGAGGATTATTTCGATAAAAATCCATTT
 GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGC
 GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
 CTAAGGAAGAAAAGAATTAAATGACTCTTTTAAAAATCTTCATAAAAAA
 GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
 TGCTGACTATGTGTATGTTTGAAGCAGGGAAAGTAACCTTATCAGGAC
 AACCAAAACAGATTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTA
 GGAGTTCCCAAATCACCAGTTTGCTCAAAGACTATCTCATAAGGGATT
 AAATTTACCTAGTTTACCAATTACTATTACGAATTTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7906

STRAIN M732

GGAAATTGAATTTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATC
 TGAAAATTGAAGATGTTTCTATACCGCGTTCATTGGGCACACAGGTTCT
 GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCTACAAA
 AGGTGAGGTAATTTGTCGATGATTTTCTATTAAAGCAGGGGACAAGAACA
 AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTCAATTTCCA
 GAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACC
 ACAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAAGTTAGTTGGTATCAGTGAGGATTATTTCGATAAAAATCCATTT
 GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGC
 GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
 CTAAGGAAGAAAAGAATTAAATGACTCTTTTAAAAATCTTCATAAAAAA
 GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
 TGCTGACTATGTGTATGTTTGAAGCAGGGAAAGTAACCTTATCAGGAC
 AACCAAAACAGATTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTA
 GGAGTTCCCAAATCACCAGTTTGCTCAAAGACTATCTCATAAGGGATT
 AAATTTACCTAGTTTACCAATTACTATTACGAATTTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7907

STRAIN COH1

GGAAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCC
 GGCATCCTCTTTGAAGGGCGTGCCCTTTTGGACGTCAATCTGAAAATTGA
 AGATGTTTCTATACCGCGTTCATTGGGCACACAGGTTCTGGAAAATCAA
 CTATTATGCAACTTTTGAATGGTTTACATATTCTACAAAAGGTGAGGTA
 ATTGTCGATGATTTTCTATTAAAGCAGGGGACAAGAACAAGAAATCAA
 ATTTATAAGGCAAAAAGTTGGTTTAGTTTCAATTTCCAGAAAGTCAGC
 TTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACCACAAAATTTT
 GGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAAAATTAAGGTT
 AGTTGGTATCAGTGAGGATTATTTCGATAAAAATCCATTTGAACTTTCTG
 GAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGCGATGGAACCC
 AAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATCCTAAGGGAAG
 AAAAGAATTAAATGACTCTTTTAAAAATCTTCATAAAAAAGGAATGACTA
 TCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTATGCTGACTAT
 GTGTATGTTTGAAGCAGGGAAAGTAACCTTATCAGGACAACCAAAACA
 GATTTTCAAGAAGTAGAACTTTAGAAAGTAAACAATTAGGAGTTCCCA
 AAATCACCAGTTTGCTCAAAGACTATCTCATAAGGGATTAAATTTACCT
 AGTTTACCAATTACTATTACGAATTTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7908

STRAIN M781

GGAAATTGAATTTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATC
 TGAAAATTGAAGATGTTTCTATACCGCGTTCATTGGGCACACAGGTTCT
 GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCTACAAA
 AGGTGAGGTAATTTGTCGATGATTTTCTATTAAAGCAGGGGACAAGAACA
 AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTCAATTTCCA
 GAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACC
 ACAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAAGTTAGTTGGTATCAGTGAGGATTATTTCGATAAAAATCCATTT
 GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGC
 GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
 CTAAGGAAGAAAAGAATTAAATGACTCTTTTAAAAATCTTCATAAAAAA
 GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
 TGCTGACTATGTGTATGTTTGAAGCAGGGAAAGTAACCTTATCAGGAC
 AACCAAAACAGATTTTCAAGAAGTAGAACTTTAGAAAGTAAACAATTA
 GGAGTTCCCAAATCACCAGTTTGCTCAAAGACTATCTCATAAGGGATT
 AAATTTACCTAGTTTACCAATTACTATTACGAATTTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7909

STRAIN CJB110

GGAAATTGAATTTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATC

Table 79: Comparative Sequences relating to SAG2150

TGAAAATGAAGATGCTTCTATACCGCGTTTCATTGGGCACACAGGTTCT
 GGAATTAACATATTATGCACTTTTGAATGGTTTACATATTCTTACAAA
 AGGTGAGGTAATGTGCGATGATTTTCTATTAAAGCAGGGGACAAGAAC
 AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTAGTTTTCAATTTCCA
 GAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACC
 ACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAATCCATT
 GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGC
 GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
 CTAAGGGAAGAAAAGAAATTAATGACTCTTTTAAAAATCTTCATAAAAAA
 GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
 TGTGACTATGTGTATGTTTAGAAGCAGGGAAAGTAACCTTATCAGGAC
 AACCAAAACAGATTTTCAAGAAGTAGAAGTTTGAAGAGTAAACAATTA
 GGAGTTCCCAAAATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGATT
 AAATTTACCTAGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7910

STRAIN 1169NT

GGAATGAATTTAAAAATGTAA

GTATACCTATCAAGCCGGCACTCTTTTGAAGGGCGTGCCCTTTTGGAC
 GTCAATCTGAAAATGAAGATGCTTCTATACCGCGTTTCATTGGGCACAC
 AGGTTCTGGAATAATCAACTATTATGCAACTTTTGAATGGTTTACATATT
 CTACAAAAGGTGAGGTAATTTGTGCGATGATTTTCTATTAAAGCAGGGGAC
 AAGAACAAGAAATCAAATTTATAAGGCAAAAAGTTGGTTAGTTTTCA
 ATTTCCAGAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTT
 TTGGACACACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCT
 GAAGAAAAATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAA
 TCCATTTGAACCTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTA
 TTTTAGCGATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGA
 CTTGATCTTAAGGGAAGAAAAGAAATTAATGACTCTTTTAAAAATCTTCA
 TAAAAAAGGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAG
 CGGATTATGCTGACTATGTGTATGTTTAGAAGCAGGGAAAGTAACCTTA
 TCAGGACCAACCAAAACAGATTTTCAAGAAGTAGAAGTTTGAAGAGTAA
 ACAATTAGGAGTTCCCAAAATCACCAGTTTGTCTCAAAGACTATCTCATA
 AGGGATTAAATTTACCTAGTTTACCAATTACTATTAAACGAATTTGTGGAG
 GCTATTAAAGCATGGA

SEQ ID NO. 7911

STRAIN JM9130013

GGAATGAATTTAAAAATGTAAAGTT

ATACCTATCAAGCCGGCACTCTTTTGAAGGGCGTGCCCTTTTGGACGTT
 AATCTGAAAATGAAGATGCTTCTATACCGCATTTCATTGGGCACACAGG
 TTCTGGAATAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCTTA
 CAAAAGGTGAGGTAATTTGTGCGATGATTTTCTATTAAAGCAGGGGACAAG
 AACAAAGAAATCAAATTTATAAGGCAAAAAGTTGGTTAGTTTTTCAATT
 TCCAGAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTG
 GACCACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAA
 GAAAAATTAAGGTTAGTTGGTATTAGTGAGGATTTATTCGATAAAAATCC
 ATTGAAGCTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTT
 TAGCGATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTT
 GATCTTAAGGGAAGAAAAGAAATTAATGACTCTTTTAAAAATCTTCATAA
 AAAAGGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGG
 ATTATGCTGACTATGTGTATGTTTAGAAGCAGGGAAAGTAACCTTATCA
 GGACAACCAAAACAGATTTTCAAGAAGTAGAAGTTTGAAGAGTAAACA
 ATTAGGAGTTCCCAAAATCACCAGTTTGTCTCAAAGACTATCTCATAAGG
 GATTAAATTTACCTAGTTTACCAATTACTATTAAACGAATTTGTGGAGGCT
 ATTAAGCATGGA

PRETTY of: /biotmp/msa238454.2{*} May 14, 2003 06:55 ..

	1		50
msa238454.2{401_A909}	---GGAATTG AATTTAAAAA	TGTAAGTTAT ACCTATCAAG	CCGGCACTCC
msa238454.2{401_H36B}	---GGAATTG AATTTAAAAA	TGTAAGTTAT ACCTATCAAG	CCGGCACTCC
msa238454.2{401_090}	---GGAATTG AATTTAAAAA	TGTAAGTTAT ACCTATCAAG	CCGGCACTCC
msa238454.2{401_1169NT}	---GGAATTG AATTTAAAAA	TGTAAGTTAT ACCTATCAAG	CCGGCACTCC
msa238454.2{401_18RS21}	---GGAATTG AATTTAAAAA	TGTAAGTTAT ACCTATCAAG	CCGGCACTCC
msa238454.2{401_2603}	atgGGAATTG AATTTAAAAA	TGTAAGTTAT ACCTATCAAG	CCGGCACTCC
msa238454.2{401_CJB110}	---GGAATTG AATTTAAAAA	TGTAAGTTAT ACCTATCAAG	CCGGCACTCC
msa238454.2{401_COH1}	---GGAATTG AATTTAAAAA	TGTAAGTTAT ACCTATCAAG	CCGGCACTCC
msa238454.2{401_M732}	---GGAATTG AATTTAAAAA	TGTAAGTTAT ACCTATCAAG	CCGGCACTCC
msa238454.2{401_M781}	---GGAATTG AATTTAAAAA	TGTAAGTTAT ACCTATCAAG	CCGGCACTCC
msa238454.2{401_JM9130013}	---GGAATTG AATTTAAAAA	TGTAAGTTAT ACCTATCAAG	CCGGCACTCC
Consensus	*****	*****	*****
	51		100
msa238454.2{401_A909}	TTTTGAAGGG CGTGCCCTTT	TTGACGTcAA TCTGAAAATT	GAAGATGcTT
msa238454.2{401_H36B}	TTTTGAAGGG CGTGCCCTTT	TTGACGTcAA TCTGAAAATT	GAAGATGcTT
msa238454.2{401_090}	TTTTGAAGGG CGTGCCCTTT	TTGACGTcAA TCTGAAAATT	GAAGATGcTT
msa238454.2{401_1169NT}	TTTTGAAGGG CGTGCCCTTT	TTGACGTcAA TCTGAAAATT	GAAGATGcTT
msa238454.2{401_18RS21}	TTTTGAAGGG CGTGCCCTTT	TTGACGTcAA TCTGAAAATT	GAAGATGcTT
msa238454.2{401_2603}	TTTTGAAGGG CGTGCCCTTT	TTGACGTcAA TCTGAAAATT	GAAGATGcTT
msa238454.2{401_CJB110}	TTTTGAAGGG CGTGCCCTTT	TTGACGTcAA TCTGAAAATT	GAAGATGcTT

Table 79: Comparative Sequences relating to SAG2150

msa238454.2{401_COH1}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTcAA	TCTGAAAAAT	GAAGATGtTT
msa238454.2{401_M732}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTcAA	TCTGAAAAAT	GAAGATGtTT
msa238454.2{401_M781}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTcAA	TCTGAAAAAT	GAAGATGtTT
msa238454.2{401_JM9130013}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTcAA	TCTGAAAAAT	GAAGATGcTT
Consensus	*****	*****	*****_*	*****	*****_*
msa238454.2{401_A909}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAAATC	AACTATTATG
msa238454.2{401_H36B}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAAATC	AACTATTATG
msa238454.2{401_090}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAAATC	AACTATTATG
msa238454.2{401_1169NT}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAAATC	AACTATTATG
msa238454.2{401_18RS21}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAAATC	AACTATTATG
msa238454.2{401_2603}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAAATC	AACTATTATG
msa238454.2{401_CJB110}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAAATC	AACTATTATG
msa238454.2{401_COH1}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAAATC	AACTATTATG
msa238454.2{401_M732}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAAATC	AACTATTATG
msa238454.2{401_M781}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAAATC	AACTATTATG
msa238454.2{401_JM9130013}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAAATC	AACTATTATG
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_H36B}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_090}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_1169NT}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_18RS21}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_2603}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_CJB110}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_COH1}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_M732}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_M781}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_JM9130013}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_H36B}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_090}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_1169NT}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_18RS21}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_2603}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_CJB110}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_COH1}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_M732}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_M781}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_JM9130013}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGGAA
msa238454.2{401_H36B}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGGAA
msa238454.2{401_090}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGGAA
msa238454.2{401_1169NT}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGGAA
msa238454.2{401_18RS21}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGGAA
msa238454.2{401_2603}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGGAA
msa238454.2{401_CJB110}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGGAA
msa238454.2{401_COH1}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGGAA
msa238454.2{401_M732}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGGAA
msa238454.2{401_M781}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGGAA
msa238454.2{401_JM9130013}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGGAA
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGGG	CCACAAAATT	TTGGTATTTC
msa238454.2{401_H36B}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGGG	CCACAAAATT	TTGGTATTTC
msa238454.2{401_090}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGGG	CCACAAAATT	TTGGTATTTC
msa238454.2{401_1169NT}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGGG	CCACAAAATT	TTGGTATTTC
msa238454.2{401_18RS21}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGGG	CCACAAAATT	TTGGTATTTC
msa238454.2{401_2603}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGGG	CCACAAAATT	TTGGTATTTC
msa238454.2{401_CJB110}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGGG	CCACAAAATT	TTGGTATTTC
msa238454.2{401_COH1}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGGG	CCACAAAATT	TTGGTATTTC
msa238454.2{401_M732}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGGG	CCACAAAATT	TTGGTATTTC
msa238454.2{401_M781}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGGG	CCACAAAATT	TTGGTATTTC
msa238454.2{401_JM9130013}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGGG	CCACAAAATT	TTGGTATTTC
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAAG	TTAGTTGGTA
msa238454.2{401_H36B}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAAG	TTAGTTGGTA
msa238454.2{401_090}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAAG	TTAGTTGGTA
msa238454.2{401_1169NT}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAAG	TTAGTTGGTA
msa238454.2{401_18RS21}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAAG	TTAGTTGGTA
msa238454.2{401_2603}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAAG	TTAGTTGGTA

Table 79: Comparative Sequences relating to SAG2150

msa238454.2{401_CJB110}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_COH1}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_M732}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_M781}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_JM9130013}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAAC TTTC	TGGAGGGCAG
msa238454.2{401_H36B}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAAC TTTC	TGGAGGGCAG
msa238454.2{401_090}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAAC TTTC	TGGAGGGCAG
msa238454.2{401_1169NT}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAAC TTTC	TGGAGGGCAG
msa238454.2{401_18RS21}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAAC TTTC	TGGAGGGCAG
msa238454.2{401_2603}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAAC TTTC	TGGAGGGCAG
msa238454.2{401_CJB110}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAAC TTTC	TGGAGGGCAG
msa238454.2{401_COH1}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAAC TTTC	TGGAGGGCAG
msa238454.2{401_M732}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAAC TTTC	TGGAGGGCAG
msa238454.2{401_M781}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAAC TTTC	TGGAGGGCAG
msa238454.2{401_JM9130013}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAAC TTTC	TGGAGGGCAG
Consensus	*-*****	*****	*****	*****	*****
msa238454.2{401_A909}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_H36B}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_090}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_1169NT}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_18RS21}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_2603}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_CJB110}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_COH1}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_M732}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_M781}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_JM9130013}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	AGTACTaGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_H36B}	AGTACTaGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_090}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_1169NT}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_18RS21}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_2603}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_CJB110}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_COH1}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_M732}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_M781}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_JM9130013}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
Consensus	*****-***	*****	*****	*****	*****
msa238454.2{401_A909}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_H36B}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_090}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_1169NT}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_18RS21}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_2603}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_CJB110}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_COH1}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_M732}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_M781}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_JM9130013}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_H36B}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_090}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_1169NT}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_18RS21}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_2603}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_CJB110}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_COH1}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_M732}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_M781}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_JM9130013}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	TTTGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAag	CAGATTTTTC
msa238454.2{401_H36B}	TTTGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAag	CAGATTTTTC
msa238454.2{401_090}	TTTGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAa	CAGATTTTTC
msa238454.2{401_1169NT}	TTTGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAa	CAGATTTTTC
msa238454.2{401_18RS21}	TTTGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAa	CAGATTTTTC

Table 79: Comparative Sequences relating to SAG2150

msa238454.2{401_2603}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTC
msa238454.2{401_CJB110}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTC
msa238454.2{401_COH1}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTC
msa238454.2{401_M732}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTC
msa238454.2{401_JM9130013}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTC
Consensus	*****	*****	*****	*****	*****
701					
msa238454.2{401_A909}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_H36B}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_090}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_1169NT}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_18RS21}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_2603}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_CJB110}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_COH1}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_M732}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_M781}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_JM9130013}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
Consensus	*****	*****	*****	*****	*****
751					
msa238454.2{401_A909}	AAGTTTGCTC	AAAGgCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_H36B}	AAGTTTGCTC	AAAGgCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_090}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_1169NT}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_18RS21}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_2603}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_CJB110}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_COH1}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_M732}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_M781}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_JM9130013}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
Consensus	*****	*****	*****	*****	*****
801					
msa238454.2{401_A909}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_H36B}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_090}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_1169NT}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_18RS21}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_2603}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_CJB110}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_COH1}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_M732}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_M781}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_JM9130013}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
Consensus	*****	*****	*****	*****	
840					
SEQ ID NO. 7912					
STRAIN 2603 frame: 1					
MGIEFKNVSYTYQAGTFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK					
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFISQIEA					
ERLAEEKLRLVIGISEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR					
KELMTLFLKNLHKKGMTIVLVTHLMDDVDYADYVYVLEAGKVTLGQPKQIFQEVELLES					
KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG					
SEQ ID NO. 7913					
STRAIN 090 frame: 1					
GIEFKNVSYTYQAGTFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK					
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFISQIEA					
ERLAEEKLRLVIGISEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR					
KELMTLFLKNLHKKGMTIVLVTHLMDDVDYADYVYVLEAGKVTLGQPKQIFQEVELLES					
KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG					
SEQ ID NO. 7914					
STRAIN 090 frame: 1					
GIEFKNVSYTYQAGTFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK					
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFISQIEA					
ERLAEEKLRLVIGISEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR					
KELMTLFLKNLHKKGMTIVLVTHLMDDVDYADYVYVLEAGKVTLGQPKQIFQEVELLES					
KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG					
SEQ ID NO. 7915					
STRAIN H36B frame: 1					
GIEFKNVSYTYQAGTFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK					
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFISQIEA					
ERLAEEKLRLVIGISEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR					
KELMTLFLKNLHKKGMTIVLVTHLMDDVDYADYVYVLEAGKVTLGQPKQIFQEVELLES					
KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG					
SEQ ID NO. 7916					

Table 79: Comparative Sequences relating to SAG2150

STRAIN 18RS21 frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTSGSKSTIMQLLNLGHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKNNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

SEQ ID NO. 7917

STRAIN M732 frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDVSYTAFIGHTSGSKSTIMQLLNLGHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKNNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

SEQ ID NO. 7918

STRAIN COH1 frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDVSYTAFIGHTSGSKSTIMQLLNLGHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKNNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

SEQ ID NO. 7919

STRAIN M781 frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDVSYTAFIGHTSGSKSTIMQLLNLGHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKNNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

SEQ ID NO. 7920

STRAIN CJB110 frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTSGSKSTIMQLLNLGHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKNNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

SEQ ID NO. 7921

STRAIN 1169NT frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTSGSKSTIMQLLNLGHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKNNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

SEQ ID NO. 7922

STRAIN JM9130013 frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTSGSKSTIMQLLNLGHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKNNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

PRETTY of: /biotmp/msa238553.2{*} May 14, 2003 06:55 ..

	1		50
msa238553.2{401_090}	~GIEFKNVSY	TYQAGTPFEG	RALFDVNLKI
msa238553.2{401_1169NT}	~GIEFKNVSY	TYQAGTPFEG	RALFDVNLKI
msa238553.2{401_18RS21}	~GIEFKNVSY	TYQAGTPFEG	RALFDVNLKI
msa238553.2{401_2603}	mGIEFKNVSY	TYQAGTPFEG	RALFDVNLKI
msa238553.2{401_CJB110}	~GIEFKNVSY	TYQAGTPFEG	RALFDVNLKI
msa238553.2{401_H36B}	~GIEFKNVSY	TYQAGTPFEG	RALFDVNLKI
msa238553.2{401_JM9130013}	~GIEFKNVSY	TYQAGTPFEG	RALFDVNLKI
msa238553.2{401_COH1}	~GIEFKNVSY	TYQAGTPFEG	RALFDVNLKI
msa238553.2{401_M732}	~GIEFKNVSY	TYQAGTPFEG	RALFDVNLKI
msa238553.2{401_M781}	~GIEFKNVSY	TYQAGTPFEG	RALFDVNLKI
Consensus	*****	*****	*****
	51		100
msa238553.2{401_090}	QLLNLGHIPT	KGEVIVDDFS	IKAGDKNKEI
msa238553.2{401_1169NT}	QLLNLGHIPT	KGEVIVDDFS	IKAGDKNKEI
msa238553.2{401_18RS21}	QLLNLGHIPT	KGEVIVDDFS	IKAGDKNKEI
msa238553.2{401_2603}	QLLNLGHIPT	KGEVIVDDFS	IKAGDKNKEI
msa238553.2{401_CJB110}	QLLNLGHIPT	KGEVIVDDFS	IKAGDKNKEI
msa238553.2{401_H36B}	QLLNLGHIPT	KGEVIVDDFS	IKAGDKNKEI
msa238553.2{401_JM9130013}	QLLNLGHIPT	KGEVIVDDFS	IKAGDKNKEI
msa238553.2{401_COH1}	QLLNLGHIPT	KGEVIVDDFS	IKAGDKNKEI
msa238553.2{401_M732}	QLLNLGHIPT	KGEVIVDDFS	IKAGDKNKEI
msa238553.2{401_M781}	QLLNLGHIPT	KGEVIVDDFS	IKAGDKNKEI

Table 79: Comparative Sequences relating to SAG2150

Consensus	*****	*****	*****	*****	*****
	101				150
msa238553.2{401_090}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_1169NT}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_18RS21}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_2603}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_CJB110}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_H36B}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_JM9130013}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_COH1}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_M732}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_M781}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
Consensus	*****	*****	*****	*****	*****
	151				200
msa238553.2{401_090}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_1169NT}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_18RS21}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_2603}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_CJB110}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_H36B}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_JM9130013}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_COH1}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_M732}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_M781}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
Consensus	*****	*****	*****	*****	*****
	201				250
msa238553.2{401_090}	VTHLMDDVAD	YADYVYVLEA	GKVTLGSGQPK	QIFQEVLELLE	SKQLGVPKIT
msa238553.2{401_1169NT}	VTHLMDDVAD	YADYVYVLEA	GKVTLGSGQPK	QIFQEVLELLE	SKQLGVPKIT
msa238553.2{401_18RS21}	VTHLMDDVAD	YADYVYVLEA	GKVTLGSGQPK	QIFQEVLELLE	SKQLGVPKIT
msa238553.2{401_2603}	VTHLMDDVAD	YADYVYVLEA	GKVTLGSGQPK	QIFQEVLELLE	SKQLGVPKIT
msa238553.2{401_CJB110}	VTHLMDDVAD	YADYVYVLEA	GKVTLGSGQPK	QIFQEVLELLE	SKQLGVPKIT
msa238553.2{401_H36B}	VTHLMDDVAD	YADYVYVLEA	GKVTLGSGQPK	QIFQEVLELLE	SKQLGVPKIT
msa238553.2{401_JM9130013}	VTHLMDDVAD	YADYVYVLEA	GKVTLGSGQPK	QIFQEVLELLE	SKQLGVPKIT
msa238553.2{401_COH1}	VTHLMDDVAD	YADYVYVLEA	GKVTLGSGQPK	QIFQEVLELLE	SKQLGVPKIT
msa238553.2{401_M732}	VTHLMDDVAD	YADYVYVLEA	GKVTLGSGQPK	QIFQEVLELLE	SKQLGVPKIT
msa238553.2{401_M781}	VTHLMDDVAD	YADYVYVLEA	GKVTLGSGQPK	QIFQEVLELLE	SKQLGVPKIT
Consensus	*****	*****	*****	*****	*****
	251				280
msa238553.2{401_090}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_1169NT}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_18RS21}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_2603}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_CJB110}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_H36B}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_JM9130013}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_COH1}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_M732}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_M781}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
Consensus	*****	*****	*****		

Table 80: Comparative Sequences relating to SAG1266

SEQ ID NO. 8001

STRAIN 2603

GTGAACCACTTACTTAACTCAGTAAAGAAAATATAGCTAAAATAGATTTTGACTTTCTT
 AATGAGGCACCTTAATGCAAAATATTCGTTTGAAAGAATTAGTAGATGAACATAAAATTTCA
 AAAGAACTGGACAGTAAAGGTTGGTCCAAAAAGACTCTCGAACGATAAAAAATCTTGATAC
 GATGGCCTTATCAATAACATATAGTTTCCCTAGATCGTGCAGATTATAACATTATCCAA
 GTCATTCCATTGCTAATGTACATGTACTACTGTTTTTAATACCAGAAAGGAGAAATCT
 AAAAATTATAGAAATACAACTACAGTGATTATGAAATGGAGTTAATCAATGAGGATAGG
 CAACAATTTTCAAAATATGAAACAGTTGATTTAGACCAATTGATACTTGTGTATATTTT
 AATATTGATGACTACATTTTCATCATATTTAACAATA

SEQ ID NO. 8002

STRAIN H36B

AACCACTTACTTAACTCAGTAAAGAAAATATAGCT
 AAAATAGATTTTGACTTTCTTAATGAGGCACCTTAATGCAAAATATTCGTTT
 GAAAGAAATTAGTAGATGAACATAAAATTTCAAAGAAGCTGGACAGTAAAG
 GTTGGTCCAAAAAGACTCTCGAACGATAAAAAATCTTGATACGATGGCCCT
 ATCAATAAACATATAGTTTCCCTAGATCGTGCAGATTATAACATTATCCA
 AGTCATTCCATTGCTAATGTACATGTACTACTGTTTTTAATACCAGAAA
 GGGAGAAATCTAAAAATTATAGAAATATACAACTACAGTGATTATGAAATG
 GAGTTAATCAATGAGGATAGGCAACAATTTTCAAAATATGAAACAGTTGA
 TTTAGACCAATTGATACTTGTGTATATTTTAATATTGATGACTACATT
 CATCATATTTAACAATA

SEQ ID NO. 8003

STRAIN 18RS21

AACCACTTACTTAACTCAGTAAAGAAAATATAG
 CTAAAAATAGATTTTGACTTTCTTAATGAGGCACCTTAATGCAAAATATTCGTT
 TTGAAAGAAATTAGTAGATGAACATAAAATTTCAAAGAAGCTGGACAGTAA
 AGGTTGGTCCAAAAAGACTCTCGAACGATAAAAAATCTTGATACGATGGCC
 TTATCAATAAACATATAGTTTCCCTAGATCGTGCAGATTATAACATTATC
 CAAGTCATTCCATTGCTAATGTACATGTACTACTGTTTTTAATACCAGA
 AAGGGAGAAATCTAAAAATTATAGAAATATACAACTACAGTGATTATGAAA
 TGGAGTTAATCAATGAGGATAGGCAACAATTTTCAAAATATGAAACAGTT
 GATTTAGACCAATTGATACTTGTGTATATTTTAATATTGATGACTACAT
 TTCATCATATTTAACAATA

PRETTY of: /biotmp/msa49308.2{*} February 19, 2003 07:45 ..

	1		50
msa49308.2{408_18RS21}	---AACCACCT	TACTTAACTC	CAGTAAAGAA
msa49308.2{408_2603}	gtgAACCACCT	TACTTAACTC	CAGTAAAGAA
msa49308.2{408_H36B}	---AACCACCT	TACTTAACTC	CAGTAAAGAA
Consensus	*****	*****	*****
	51		100
msa49308.2{408_18RS21}	TGACTTTCTT	AATGAGGCAC	TTAATGCAAA
msa49308.2{408_2603}	TGACTTTCTT	AATGAGGCAC	TTAATGCAAA
msa49308.2{408_H36B}	TGACTTTCTT	AATGAGGCAC	TTAATGCAAA
Consensus	*****	*****	*****
	101		150
msa49308.2{408_18RS21}	TAGATGAACCT	AAAAATTTCA	AAAGAACTGG
msa49308.2{408_2603}	TAGATGAACCT	AAAAATTTCA	AAAGAACTGG
msa49308.2{408_H36B}	TAGATGAACCT	AAAAATTTCA	AAAGAACTGG
Consensus	*****	*****	*****
	151		200
msa49308.2{408_18RS21}	AAAGACTCTC	GAACGATAAA	AATCTTGTAC
msa49308.2{408_2603}	AAAGACTCTC	GAACGATAAA	AATCTTGTAC
msa49308.2{408_H36B}	AAAGACTCTC	GAACGATAAA	AATCTTGTAC
Consensus	*****	*****	*****
	201		250
msa49308.2{408_18RS21}	TATAGTTTCC	CTAGATCGTG	CAGATTATAA
msa49308.2{408_2603}	TATAGTTTCC	CTAGATCGTG	CAGATTATAA
msa49308.2{408_H36B}	TATAGTTTCC	CTAGATCGTG	CAGATTATAA
Consensus	*****	*****	*****
	251		300
msa49308.2{408_18RS21}	TTGCTAATGT	ACATGTACTA	CTGTTTTTAA
msa49308.2{408_2603}	TTGCTAATGT	ACATGTACTA	CTGTTTTTAA
msa49308.2{408_H36B}	TTGCTAATGT	ACATGTACTA	CTGTTTTTAA
Consensus	*****	*****	*****
	301		350
msa49308.2{408_18RS21}	AAAAATTATA	GAATATACAA	CTACAGTGAT
msa49308.2{408_2603}	AAAAATTATA	GAATATACAA	CTACAGTGAT
msa49308.2{408_H36B}	AAAAATTATA	GAATATACAA	CTACAGTGAT
Consensus	*****	*****	*****

Table 80: Comparative Sequences relating to SAG1266

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351                                     400
msa49308.2{408_18RS21} TGAGGATAGG CAACAATTTT CAAAATATGA AACAGTTGAT TTAGACCAAT
msa49308.2{408_2603} TGAGGATAGG CAACAATTTT CAAAATATGA AACAGTTGAT TTAGACCAAT
msa49308.2{408_H36B} TGAGGATAGG CAACAATTTT CAAAATATGA AACAGTTGAT TTAGACCAAT
Consensus *****

401                                     450
msa49308.2{408_18RS21} TGATACTTGT TGATATTTT AATATTGATG ACTACATTTC ATCATATTTA
msa49308.2{408_2603} TGATACTTGT TGATATTTT AATATTGATG ACTACATTTC ATCATATTTA
msa49308.2{408_H36B} TGATACTTGT TGATATTTT AATATTGATG ACTACATTTC ATCATATTTA
Consensus *****

451
msa49308.2{408_18RS21} ACAATA
msa49308.2{408_2603} ACAATA
msa49308.2{408_H36B} ACAATA
Consensus *****

SEQ ID NO. 8004
STRAIN 2603 frame: 1
VNHLNLSKENIAKIDFDLNEALNANIRLKELVDELKISKELDSKGWSKKDSRTIKILY
DGLINKHIVSLDRADYNI IQVIPFANVHVLFLIPERENSKNYRIYNYSYEMELINEDR
QQFSKYETVDLDQLILVDIFNIDDISSYLTII

SEQ ID NO. 8005
STRAIN H36B frame: 1
NHLLNLSKENIAKIDFDLNEALNANIRLKELVDELKISKELDSKGWSKKDSRTIKILYD
GLINKHIVSLDRADYNI IQVIPFANVHVLFLIPERENSKNYRIYNYSYEMELINEDRQ
QQFSKYETVDLDQLILVDIFNIDDISSYLTII

SEQ ID NO. 8006
STRAIN 18RS21 frame: 1
NHLLNLSKENIAKIDFDLNEALNANIRLKELVDELKISKELDSKGWSKKDSRTIKILYD
GLINKHIVSLDRADYNI IQVIPFANVHVLFLIPERENSKNYRIYNYSYEMELINEDRQ
QQFSKYETVDLDQLILVDIFNIDDISSYLTII

PRETTY of: /biotmp/msa49418.2{*} February 19, 2003 07:47 ..

1                                     50
msa49418.2{408_18RS21} -NHLLNLSKE NIAKIDFDL NEALNANIRL KELVDELKIS KELDSKGWSK
msa49418.2{408_2603} vNHLLNLSKE NIAKIDFDL NEALNANIRL KELVDELKIS KELDSKGWSK
msa49418.2{408_H36B} -NHLLNLSKE NIAKIDFDL NEALNANIRL KELVDELKIS KELDSKGWSK
Consensus *****

51                                     100
msa49418.2{408_18RS21} KDSRTIKILY DGLINKHIVS LDRADYNI IQ VIPFANVHVL LFLIPERENS
msa49418.2{408_2603} KDSRTIKILY DGLINKHIVS LDRADYNI IQ VIPFANVHVL LFLIPERENS
msa49418.2{408_H36B} KDSRTIKILY DGLINKHIVS LDRADYNI IQ VIPFANVHVL LFLIPERENS
Consensus *****

101                                    150
msa49418.2{408_18RS21} KNYRIYNYS YEMELINEDR QQFSKYETVD LDQLILVDIF NIDDISSYL
msa49418.2{408_2603} KNYRIYNYS YEMELINEDR QQFSKYETVD LDQLILVDIF NIDDISSYL
msa49418.2{408_H36B} KNYRIYNYS YEMELINEDR QQFSKYETVD LDQLILVDIF NIDDISSYL
Consensus *****

151
msa49418.2{408_18RS21} TI
msa49418.2{408_2603} TI
msa49418.2{408_H36B} TI
Consensus **

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Table 81: Comparative Sequences relating to SAG0011

SEQ ID NO. 8101

STRAIN 090

AGCAAGCCTAATGTTGTTTCAGTTAAA
 TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATG
 CTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTTT
 ACAAGAACGTCGTCAAGAAGTTGTAAAAATTAACGAAAGACTATCAGACAT
 TAACTAATAGAACTGAGAACCAGAAGTTGCTAGCAAAACAATAAAAAAT
 CCAGATTACGTTCAAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
 CGCGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8102

STRAIN A909

AGCAAGCCTAATGTTGTTTCAGTTAAATAATCAATA
 TATTAAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGGAGTTACGCCGAAAAAATCG
 TTTAATGGGTTGGGTTCTTATTTTGTCTATGCTtttATTTATTTTACCCACTTATAATTT
 AGTTAAGAGTTACAGAACCTTACAAGAAGTCGTCAAGAAGTTGTAAAAATTAACGAAAGA
 CTATCAGACATTAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAATAAAAAA
 TCCAGATTACGTTCAAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGACCGCGAAAT
 GATTTACCCATTACCAGACCT

SEQ ID NO. 8103

STRAIN H36B

AGCAAGCCTAATGTTGTTTCAGTTAAA
 TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATG
 CTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTTT
 ACAAGAACGTCGTCAAGAAGTTGTAAAAATTAACGAAAGACTATCAGACAT
 TAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAATAAAAAAT
 CCAGATTACGTTCAAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
 CGCGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8104

STRAIN 18RS21

AGCAAGCCTAATGTTGTTTCAGTTAAATAATCAATATATTAACGATGAGAATCTAAAAAA
 CGTTACGAAGCTGAGGAGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTT
 GTCATGCTTTTATTTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTTACAA
 GAACGTCGTCAAGAAGTTGTAAAAATTAACGAAAGACTATCAGACATTAACTAATAGAACT
 GAGAACCAGAAGTTGCTAGCAAAACAATAAAAAATCCAGATTACGTTCAAAAAATATGCT
 CGAGCTAAGTATTATTTCTCTAAGACCGCGAAATGATTTACCCATTACCAGACCTTTTA
 CCAAAA

SEQ ID NO. 8105

STRAIN M732

AGCAAGCCTAATGTTGTTTCAGTTAAA
 TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATG
 CTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTTT
 ACAAGAACGTCGTCAAGAAGTTGTAAAAATTAACGAAAGACTATCAGACAT
 TAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAATAAAAAAT
 CCAGATTACGTTCAAAAAATATGCTCGAGCGAAGTATTATTTCTCTAAGAC
 CGCGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8106

STRAIN COH1

AGCAAGCCTAATGTTGTTTCAGTTAAATAATC
 AATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGGAGTTA
 CGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATGCTttt
 ATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTTTACAAG
 AACGTCGTCAAGAAGTTGTAAAAATTAACGAAAGACTATCAGACATTAACT
 AATAGAACTGAGAACCAGAAGTTACTAGCAAAACAATAAAAAATCCAGA
 TTACGTTCAAAAAATATGCTCGAGCGAAGTATTATTTCTCTAAGACCGCG
 AATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8107

STRAIN M781

AGCaAGCCTAATGTTGTTTCAGTT
 AAATAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTG
 AGGAGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCT
 ATGCTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAAC
 TTTACAAGAAGTCGTCAAGAAGTTGTAAAAATTAACGAAAGACTATCAGA
 CATTAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAATAAAA
 AATCCAGATTACGTTCAAAAAATATGCTCGAGCGAAGTATTATTTCTCTAA
 GACCGCGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8108

STRAIN CJB110

AGCAAGCCTAATGTTGTTTCAGTTAAATAATC
 AATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGGAGTTA
 CGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATGCTttt
 ATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTTTACAAG

Table 81: Comparative Sequences relating to SAG0011

AACGTCGTCAGAAAGTTGTAAAATTAACGAAAGACTATCAGACATTAAC
 AATAGAACTGAGAACCCAGAAGTTGCTAGCAAAACAACTAAAAATCCAGA
 TTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTTAAGACCGGCG
 AAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8109

STRAIN 1169NT

AGCAAGCCTAATGTTTTCAGTTAAA
 TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATG
 CTTTTATTTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTT
 ACAAGAAGCTCGTCAAGAAAGTTGTAAAATTAACGAAAGACTATCAGACAT
 TAACTAATAGAACTGAGAACCCAGAAGTTACTAGCAAAACAACTAAAAAT
 CCGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
 CGCGGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8110

STRAIN JM9130013

AGCAAGCCTAATGTTTTCAGTTAAA
 TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATG
 CTTTTATTTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTT
 ACAAGAAGCTCGTCAAGAAAGTTGTAAAATTAACGAAAGACTATCAGACAT
 TAACTAATAGAACTGAGAACCCAGAAGTTACTAGCAAAACAACTAAAAAT
 CCGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
 TGGCGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8111

STRAIN 2603

agcaagcctaagtgtgttcagttaataatcaatatattaacgatgagaa
 tctaaaaaacgttacgaagctgaggagttacgccgaaaaaatcgtttaa
 tgggttgggttcttattttgtcatgcttttatttttaccacttat
 aatttagttaagagttacagaactttacaagaagctcgtaagaagttgt
 aaaattaacgaagactatcagacattaactaatagaactgagaaccaga
 agttgctagcaaaacaactaaaaatccagattacgttcaaaaatgatgct
 cgagctaagttattttcttaagaccggcgaaatgatttaccattacc
 agaccttttaccaaaa

PRETTY of: /biotmp/msa25643.2{*} . April 29, 2002 05:59 ..

	1		50
msa25643.2{418_COH1}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_M732}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_M781}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_JM9130013}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_090}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_18RS21}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_2603}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_CJB110}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_1169NT}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_A909}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_H36B}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
Consensus	*****	*****	*****
	51		100
msa25643.2{418_COH1}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_M732}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_M781}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_JM9130013}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_090}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_18RS21}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_2603}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_CJB110}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_1169NT}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_A909}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_H36B}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
Consensus	*****	*****	*****
	101		150
msa25643.2{418_COH1}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_M732}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_M781}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_JM9130013}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_090}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_18RS21}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_2603}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_CJB110}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_1169NT}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_A909}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_H36B}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
Consensus	*****	*****	*****

Table 81: Comparative Sequences relating to SAG0011

		151			200	
msa25643.2{418_COH1}		AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_M732}		AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_M781}		AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_JM9130013}		AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_090}		AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_18RS21}		AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_2603}		AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_CJB110}		AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_1169NT}		AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_A909}		AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_H36B}		AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
Consensus		*****	*****	*****	*****	*****
		201			250	
msa25643.2{418_COH1}		AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_M732}		AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_M781}		AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_JM9130013}		AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_090}		AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_18RS21}		AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_2603}		AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_CJB110}		AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_1169NT}		AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_A909}		AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_H36B}		AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
Consensus		*****	*****	*****	*****	*****
		251			300	
msa25643.2{418_COH1}		AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_M732}		AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_M781}		AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_JM9130013}		AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_090}		AGTTgCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_18RS21}		AGTTgCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_2603}		AGTTgCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_CJB110}		AGTTgCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_1169NT}		AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_A909}		AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_H36B}		AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
Consensus		****-****	*****	*****	*****	*****
		301			350	
msa25643.2{418_COH1}		CGAGCgAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_M732}		CGAGCgAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_M781}		CGAGCgAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_JM9130013}		CGAGCgAAGT	ATTATTTCTC	TAAGACtGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_090}		CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_18RS21}		CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_2603}		CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_CJB110}		CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_1169NT}		CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_A909}		CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_H36B}		CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
Consensus		*****-****	*****	*****-****	*****	*****
		351	366			
msa25643.2{418_COH1}		AGACCTTttaa	ccaaaa			
msa25643.2{418_M732}		AGACCTTttaa	ccaaaa			
msa25643.2{418_M781}		AGACCTTttaa	ccaaaa			
msa25643.2{418_JM9130013}		AGACCTTttaa	ccaaaa			
msa25643.2{418_090}		AGACCTTttaa	ccaaaa			
msa25643.2{418_18RS21}		AGACCTTttaa	ccaaaa			
msa25643.2{418_2603}		AGACCTTttaa	ccaaaa			
msa25643.2{418_CJB110}		AGACCTTttaa	ccaaaa			
msa25643.2{418_1169NT}		AGACCTTttaa	ccaaaa			
msa25643.2{418_A909}		AGACCT~~~~~	~~~~~			
msa25643.2{418_H36B}		AGACCTTttaa	ccaaaa			
Consensus		*****-----	-----			

SEQ ID NO. 8112

STRAIN 090

SKPNVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVKLTKDYQTLTNRTNENQKLLAKQLKNPDYVQKYARAKYFSKTGEM
 IYPLDLLPK

SEQ ID NO. 8113

STRAIN A909

SKPNVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVKLTKDYQTLTNRTNENQKLLAKQLKNPDYVQKYARAKYFSKTGEM

Table 81: Comparative Sequences relating to SAG0011

IYPLPD

SEQ ID NO. 8114

STRAIN H36B

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM
 IYPLPDLLPK

SEQ ID NO. 8115

STRAIN 18RS21

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNLVKSYRTLQ
 ERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM IYPLPDLL
 PK

SEQ ID NO. 8116

STRAIN M732

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM
 IYPLPDLLPK

SEQ ID NO. 8117

STRAIN COH1

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNLVK
 SYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM IY
 PLPDLLPK

SEQ ID NO. 8118

STRAIN M781

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 LVKSYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGE
 MIYPLPDLLPK

SEQ ID NO. 8119

STRAIN CJB110

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNLVK
 SYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM IY
 PLPDLLPK

SEQ ID NO. 8120

STRAIN 1169NT

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM
 IYPLPDLLPK

SEQ ID NO. 8121

STRAIN JM9130013

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM
 IYPLPDLLPK

SEQ ID NO. 8122

STRAIN 2603

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNLVKSYRTLQ
 ERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM IYPLPDLL
 PK

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa20122.2{*} April 29, 2002 06:08 ..

	1		50
msa20122.2{418_090}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK NRLMGWVLI FVMLLFILPTY	
msa20122.2{418_A909}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK NRLMGWVLI FVMLLFILPTY	
msa20122.2{418_1169NT}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK NRLMGWVLI FVMLLFILPTY	
msa20122.2{418_18RS21}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK NRLMGWVLI FVMLLFILPTY	
msa20122.2{418_2603}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK NRLMGWVLI FVMLLFILPTY	
msa20122.2{418_CJB110}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK NRLMGWVLI FVMLLFILPTY	
msa20122.2{418_COH1}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK NRLMGWVLI FVMLLFILPTY	
msa20122.2{418_H36B}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK NRLMGWVLI FVMLLFILPTY	
msa20122.2{418_JM9130013}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK NRLMGWVLI FVMLLFILPTY	
msa20122.2{418_M732}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK NRLMGWVLI FVMLLFILPTY	
msa20122.2{418_M781}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK NRLMGWVLI FVMLLFILPTY	
Consensus	*****	*****	*****
	51		100
msa20122.2{418_090}	NLVKSRYRTLQ	ERRQEVVVKLT KDYQTLTNRT ENQKLLAKQL KNPDYVQKYA	
msa20122.2{418_A909}	NLVKSRYRTLQ	ERRQEVVVKLT KDYQTLTNRT ENQKLLAKQL KNPDYVQKYA	

Table 81: Comparative Sequences relating to SAG0011

msa20122.2{418_1169NT}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_18RS21}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_2603}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_CJB110}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_COH1}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_H36B}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_JM9130013}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_M732}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_M781}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
Consensus	*****	*****	*****	*****	*****
	101		122		
msa20122.2{418_090}	RAKYFSGKTG	EMIYPLPD11	pk		
msa20122.2{418_A909}	RAKYFSGKTG	EMIYPLPD--	--		
msa20122.2{418_1169NT}	RAKYFSGKTG	EMIYPLPD11	pk		
msa20122.2{418_18RS21}	RAKYFSGKTG	EMIYPLPD11	pk		
msa20122.2{418_2603}	RAKYFSGKTG	EMIYPLPD11	pk		
msa20122.2{418_CJB110}	RAKYFSGKTG	EMIYPLPD11	pk		
msa20122.2{418_COH1}	RAKYFSGKTG	EMIYPLPD11	pk		
msa20122.2{418_H36B}	RAKYFSGKTG	EMIYPLPD11	pk		
msa20122.2{418_JM9130013}	RAKYFSGKTG	EMIYPLPD11	pk		
msa20122.2{418_M732}	RAKYFSGKTG	EMIYPLPD11	pk		
msa20122.2{418_M781}	RAKYFSGKTG	EMIYPLPD11	pk		
Consensus	*****	*****--	--		

Table 82: Comparative Sequences relating to SAG0165

SEQ ID NO. 8201

STRAIN 2603

ATGAAAAATTATTGTTAAAAATGTAAGGATAAGAAGGTTAAAGCATTTCACATTTTAGAA
 TGTTTGGTAGCATTGGTTACAATCACAGGAGCTTTACTAGTTTATCAAGGACTGACAAAA
 TTGTTGGCTCAACAGATAGTAGTGATGCTTCTCCAGTCAGTCTGAATGGGTGTTATTA
 AcTCAGCAACTAAATGCAGAATTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAAA
 CTTTATTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATTC
 CGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGGTTAGACAATTGT
 CAAATGAGTCAGACCAAAAGTATGGTAAAACTTGTTTTTATTTTAAAGGACGGGTAAAA
 AGGACATTTTACTATGATTTTAAAGAAGAACTTAA

SEQ ID NO. 8202

STRAIN 090

AATTGGAAGGCGCTCACTTGAATATTTAAGACAGAACAACTTTATTTA
 CGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATTT
 CCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGGT
 TAGACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAAACTTGTTT
 TATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAGA
 AACT

SEQ ID NO. 8203

STRAIN A909

CAGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAACTTTAT
 TTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGA
 TTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATG
 GGTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTGTT
 TTTTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGA
 AGAACT

SEQ ID NO. 8204

STRAIN H36B

ATGCAGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAACTT
 TATTTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGA
 TGATTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTT
 ATGGGTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTT
 GTTTTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAA
 AGAAGAACT

SEQ ID NO. 8205

STRAIN 18RS21

AGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAACTTTATT
 TACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAT
 TTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGG
 GTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTGTTT
 TTTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAA
 GAACT

SEQ ID NO. 8206

STRAIN M732

CAGAATTTGAAGGCGCTCACTTGAATATTTAAGACAGAACAACTTTAT
 TTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGA
 TTTCCGTAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTTATG
 GGTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTGTT
 TTTTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGA
 AGAACT

SEQ ID NO. 8207

STRAIN COH1

GAATTCGAAGGCGCTCACTTGAATATTTAAGACAGAACAACTTTATTT
 ACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAT
 TCCGTAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTTATGGG
 TTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTGTTT
 TTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAG
 AACT

SEQ ID NO. 8208

STRAIN M781

AGAATTCGAAGGCGCTCACTTGAATATTTAAGACAGAACAACTTTATT
 TACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAT
 TTCCGTAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTTATGG
 GTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTGTTT
 TTTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAA
 GAACT

SEQ ID NO. 8209

STRAIN CJB110

GAATTCGAAGGCGCTCACTTGAATATTTAAGACAGAACAACTTTATTT
 ACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAT
 TCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGG
 TTAGACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAAACTTGTTT
 TTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAG
 AACT

Table 82: Comparative Sequences relating to SAG0165

SEQ ID NO. 8210

STRAIN 1169NT

TCGAAGGCGCTCACTTGGAAATATTTAAGACAGAACAACTTTATTACGT
 AAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAGATGATTTTCG
 TAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGGTTAG
 ACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAACTTGTTTTAT
 TTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAGAAAC
 T

SEQ ID NO. 8211

STRAIN JM9130013

TGCAGAAITTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAACTTT
 ATTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAGAT
 GATTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTA
 TGGGTTAGACAAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAACTTG
 TTTTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAA
 GAAGAACT

PRETTY of: /biotmp/msa128189.2{*} February 7, 2003 08:19 ..

	1				50
msa128189.2{6_18RS21}	-----	-----	-----	-----	-----
msa128189.2{6_2603}	atgaaaaatt	tattgttaaa	atgtaaggat	aagaaggtta	aagcatttac
msa128189.2{6_A909}	-----	-----	-----	-----	-----
msa128189.2{6_H36B}	-----	-----	-----	-----	-----
msa128189.2{6_JM9130013}	-----	-----	-----	-----	-----
msa128189.2{6_COH1}	-----	-----	-----	-----	-----
msa128189.2{6_M732}	-----	-----	-----	-----	-----
msa128189.2{6_M781}	-----	-----	-----	-----	-----
msa128189.2{6_090}	-----	-----	-----	-----	-----
msa128189.2{6_CJB110}	-----	-----	-----	-----	-----
msa128189.2{6_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa128189.2{6_18RS21}	-----	-----	-----	-----	-----
msa128189.2{6_2603}	acttttagaa	tggttgtag	cattgggtac	aatcacagga	gctttactag
msa128189.2{6_A909}	-----	-----	-----	-----	-----
msa128189.2{6_H36B}	-----	-----	-----	-----	-----
msa128189.2{6_JM9130013}	-----	-----	-----	-----	-----
msa128189.2{6_COH1}	-----	-----	-----	-----	-----
msa128189.2{6_M732}	-----	-----	-----	-----	-----
msa128189.2{6_M781}	-----	-----	-----	-----	-----
msa128189.2{6_090}	-----	-----	-----	-----	-----
msa128189.2{6_CJB110}	-----	-----	-----	-----	-----
msa128189.2{6_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	101				150
msa128189.2{6_18RS21}	-----	-----	-----	-----	-----
msa128189.2{6_2603}	tttatcaagg	actgacaaaa	ttgttggtc	aacagatagt	agtgatgtct
msa128189.2{6_A909}	-----	-----	-----	-----	-----
msa128189.2{6_H36B}	-----	-----	-----	-----	-----
msa128189.2{6_JM9130013}	-----	-----	-----	-----	-----
msa128189.2{6_COH1}	-----	-----	-----	-----	-----
msa128189.2{6_M732}	-----	-----	-----	-----	-----
msa128189.2{6_M781}	-----	-----	-----	-----	-----
msa128189.2{6_090}	-----	-----	-----	-----	-----
msa128189.2{6_CJB110}	-----	-----	-----	-----	-----
msa128189.2{6_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	151				200
msa128189.2{6_18RS21}	-----	-----	-----	-----	-----
msa128189.2{6_2603}	tcttccagtc	agtctgaatg	ggtgttatta	actcagcaac	taaATGCaga
msa128189.2{6_A909}	-----	-----	-----	-----	-----
msa128189.2{6_H36B}	-----	-----	-----	-----	-----
msa128189.2{6_JM9130013}	-----	-----	-----	-----	-----
msa128189.2{6_COH1}	-----	-----	-----	-----	-----
msa128189.2{6_M732}	-----	-----	-----	-----	-----
msa128189.2{6_M781}	-----	-----	-----	-----	-----
msa128189.2{6_090}	-----	-----	-----	-----	-----
msa128189.2{6_CJB110}	-----	-----	-----	-----	-----
msa128189.2{6_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	201				250
msa128189.2{6_18RS21}	atTtGAAGGC	GCTCAtcTGG	AATATTTAAG	ACAGAACAAA	CITTATTTAC
msa128189.2{6_2603}	atTtGAAGGC	GCTCAtcTGG	AATATTTAAG	ACAGAACAAA	CITTATTTAC
msa128189.2{6_A909}	atTtGAAGGC	GCTCAtcTGG	AATATTTAAG	ACAGAACAAA	CITTATTTAC
msa128189.2{6_H36B}	atTtGAAGGC	GCTCAtcTGG	AATATTTAAG	ACAGAACAAA	CITTATTTAC

Table 82: Comparative Sequences relating to SAG0165

msa128189.2{6_JM9130013}	atTtGAAGGC	GCTCAtcTGG	AATATTTAAG	ACAGAACAAA	CTTTATTAC
msa128189.2{6_COH1}	atTcGAAGGC	GCTCActTGG	AATATTTAAG	ACAGAACAAA	CTTTATTAC
msa128189.2{6_M732}	atTcGAAGGC	GCTCActTGG	AATATTTAAG	ACAGAACAAA	CTTTATTAC
msa128189.2{6_M781}	atTcGAAGGC	GCTCActTGG	AATATTTAAG	ACAGAACAAA	CTTTATTAC
msa128189.2{6_CJB110}	atTcGAAGGC	GCTCActTGG	AATATTTAAG	ACAGAACAAA	CTTTATTAC
msa128189.2{6_1169NT}	~TcGAAGGC	GCTCActTGG	AATATTTAAG	ACAGAACAAA	CTTTATTAC
Consensus	~*~*****	*****--***	*****	*****	*****
251					
msa128189.2{6_18RS21}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTC
msa128189.2{6_2603}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTC
msa128189.2{6_A909}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTC
msa128189.2{6_H36B}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTC
msa128189.2{6_JM9130013}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTC
msa128189.2{6_COH1}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTC
msa128189.2{6_M732}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTC
msa128189.2{6_M781}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTC
msa128189.2{6_090}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTC
msa128189.2{6_CJB110}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTC
msa128189.2{6_1169NT}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTC
Consensus	*****	*****	*****	*****	*****
301					
msa128189.2{6_18RS21}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_2603}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_A909}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_H36B}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_JM9130013}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_COH1}	CGTAAGACAG	GTTATaATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_M732}	CGTAAGACAG	GTTATaATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_M781}	CGTAAGACAG	GTTATaATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_090}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_CJB110}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_1169NT}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
Consensus	*****	*****	*****	*****	*****
351					
msa128189.2{6_18RS21}	AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTITTTT
msa128189.2{6_2603}	AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTITTTT
msa128189.2{6_A909}	AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTITTTT
msa128189.2{6_H36B}	AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTITTTT
msa128189.2{6_JM9130013}	AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTITTTT
msa128189.2{6_COH1}	AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTITTTT
msa128189.2{6_M732}	AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTITTTT
msa128189.2{6_M781}	AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTITTTT
msa128189.2{6_090}	AGACAATTGT	CAAATGAGTC	AaACCAAAAG	TATGGTAAAA	CTTGTITTTT
msa128189.2{6_CJB110}	AGACAATTGT	CAAATGAGTC	AaACCAAAAG	TATGGTAAAA	CTTGTITTTT
msa128189.2{6_1169NT}	AGACAATTGT	CAAATGAGTC	AaACCAAAAG	TATGGTAAAA	CTTGTITTTT
Consensus	*****	*****	*~*****	*****	*****
401					
msa128189.2{6_18RS21}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_2603}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_A909}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_H36B}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_JM9130013}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_COH1}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_M732}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_M781}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_090}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_CJB110}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_1169NT}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
Consensus	*****	*****	*****	*****	*****
451					
msa128189.2{6_18RS21}	ACT---				
msa128189.2{6_2603}	ACTtaa				
msa128189.2{6_A909}	ACT---				
msa128189.2{6_H36B}	ACT---				
msa128189.2{6_JM9130013}	ACT---				
msa128189.2{6_COH1}	ACT---				
msa128189.2{6_M732}	ACT---				
msa128189.2{6_M781}	ACT---				
msa128189.2{6_090}	ACT---				
msa128189.2{6_CJB110}	ACT---				
msa128189.2{6_1169NT}	ACT---				
Consensus	*****				

SEQ ID NO. 8212

STRAIN 2603 frame: 1

MKNLLKCKDKKVKAFPTLLECLVALVTITGALLVYQGLTKLLAQQIVVMSSSSQSEWVLL
 TQQLNAEFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNC

Table 82: Comparative Sequences relating to SAG0165

QMSQTKSMVKLVFYFKDGLKRTFFYDFKEET.

SEQ ID NO. 8213

STRAIN 090 frame: 3

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTKS
MVKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8214

STRAIN A909 frame: 3

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8215

STRAIN H36B frame: 3

AEFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQT
KSMVKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8216

STRAIN 18RS21 frame: 2

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8217

STRAIN M732 frame: 3

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8218

STRAIN COH1 frame: 1

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8219

STRAIN M781 frame: 2

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8220

STRAIN CJB110 frame: 1

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8221

STRAIN 1169NT frame: 3

EGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTKSM
VKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8222

STRAIN JM9130013 frame: 2

AEFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQT
KSMVKLVFYFKDGLKRTFFYDFKEET

PRETTY of: /biotmp/msa128319.2{*} February 7, 2003 08:27 ..

	1				50
msa128319.2{6_090}	-----	-----	-----	-----	-----
msa128319.2{6_1169NT}	-----	-----	-----	-----	-----
msa128319.2{6_18RS21}	-----	-----	-----	-----	-----
msa128319.2{6_2603}	mknlllkckd	kkvkaftlle	clvalvtitg	allvyggltk	llaqqivvms
msa128319.2{6_H36B}	-----	-----	-----	-----	-----
msa128319.2{6_JM9130013}	-----	-----	-----	-----	-----
msa128319.2{6_A909}	-----	-----	-----	-----	-----
msa128319.2{6_CJB110}	-----	-----	-----	-----	-----
msa128319.2{6_COH1}	-----	-----	-----	-----	-----
msa128319.2{6_M732}	-----	-----	-----	-----	-----
msa128319.2{6_M781}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa128319.2{6_090}	-----	-----fEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_1169NT}	-----	-----EG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_18RS21}	-----	-----EfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_2603}	sssqsewvll	tqqlnAEfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_H36B}	-----	-----AEfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_JM9130013}	-----	-----AEfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_A909}	-----	-----EfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_CJB110}	-----	-----EfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_COH1}	-----	-----EfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_M732}	-----	-----EfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_M781}	-----	-----EfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
Consensus	*****	*****_**	*****	*****	*****

Table 82: Comparative Sequences relating to SAG0165

	101			150
msa128319.2{6_090}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK	LVFYFKDGLK RTFYFDKKEE
msa128319.2{6_1169NT}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK	LVFYFKDGLK RTFYFDKKEE
msa128319.2{6_18RS21}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK	LVFYFKDGLK RTFYFDKKEE
msa128319.2{6_2603}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK	LVFYFKDGLK RTFYFDKKEE
msa128319.2{6_H36B}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK	LVFYFKDGLK RTFYFDKKEE
msa128319.2{6_JM9130013}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK	LVFYFKDGLK RTFYFDKKEE
msa128319.2{6_A909}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK	LVFYFKDGLK RTFYFDKKEE
msa128319.2{6_CJB110}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK	LVFYFKDGLK RTFYFDKKEE
msa128319.2{6_COH1}	RKTGYnGRGY	QPMVYGLDNC	QMSQTKSMVK	LVFYFKDGLK RTFYFDKKEE
msa128319.2{6_M732}	RKTGYnGRGY	QPMVYGLDNC	QMSQTKSMVK	LVFYFKDGLK RTFYFDKKEE
msa128319.2{6_M781}	RKTGYnGRGY	QPMVYGLDNC	QMSQTKSMVK	LVFYFKDGLK RTFYFDKKEE
Consensus	*****	*****	*****	*****
	151			
msa128319.2{6_090}	T~			
msa128319.2{6_1169NT}	T~			
msa128319.2{6_18RS21}	T~			
msa128319.2{6_2603}	T~			
msa128319.2{6_H36B}	T~			
msa128319.2{6_JM9130013}	T~			
msa128319.2{6_A909}	T~			
msa128319.2{6_CJB110}	T~			
msa128319.2{6_COH1}	T~			
msa128319.2{6_M732}	T~			
msa128319.2{6_M781}	T~			
Consensus	**			

Table 83: Comparative Sequences relating to SAG0108

SEQ ID NO. 8301

STRAIN 2603

atgaaaaagattcgattatcaaagtttattaaaatgattgttattttgttttaatt
 agtgtagcagctagttttatttttccacgttgcccaagttcgagatgataaatccttt
 atttcaaatgggtcaacgttaagcctggaaactctttatatgtctatgataaatcctttgat
 aagctattaaagcaaaaaatagaaatgacaaacaaaataaaagcaagttgcttggtat
 gtctctgctgttaagaaaactcataagacagctgttgcgttcaggttttgcgaatagc
 aaagagaatatgaaggcatatgggttggtctgtttcataagttaggatataaatgttcttatg
 cctgacaatattgcacatgggtgaaagtcatgggcagttgataggctatggctggaacgac
 cgcgagaacattatcaaatggacagaaatgatagttgataagaatccatcaagccaaatt
 actttatttgggtgttcaatgggtggagcaacagtcagtgaggctagtggtgaaaaatta
 cctagtcaggtgtttaatcatctgaagattgcggttattctagtggttggatgaatta
 aaatttcaggctaaagagatgtatgggttaccagccttcccactcttatatgaagtttca
 caaatttctaaaatcagagcaggttttctgtatggacaagcaagtagtgctgaacaattg
 aaaaagaataatttaccagccctctttattcatggtgataaggataatttgtttccaaca
 agtatgggttatgacaactataaagctacagcaggttaagaaagagctttatatgtaaaa
 ggggcaaacatgcgaatcttttgaacagagccagaaaaatatgagaaacgtatctct
 agttttttgaaaaaatatgaaaaa

SEQ ID NO. 8302

STRAIN 090

GCTAGTTTTATTTTTTCCACGTTGCCCAAGTTCC
 AGATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTT
 TATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAATAGAA
 ATGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGCTAA
 GAAACTCATAAGACAGCTGTTGTCGTTTCATGGTTTTGCGAATAGCAAAAG
 AGAATATGAAGGCATATGTTGGCTGTTTCATAAGTTAGGATACAATGTT
 CTATGCTTACCAATATGACATGCTGGAAGTTCATGGGCAGTTGATAGG
 CTATGGCTGGAACGACCGGAGAACATTATCAATGGACAGAAATGATAG
 TTGATAAGAATCCATCAAGCCAAATTACTTTaTTTGGTGTTCATGGGT
 GGAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGT
 TAATATCATTTGAAGATTGCGGTTATTCTAGTGTTCGGATGAATTAAT
 TTCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCCTCTTATATGAA
 GTTTCACAAATTTCTAAATCAGAGCAGGTTTTCTGTATGGACAAGCAAG
 TAGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCATG
 GTGATAAGGATAATTTTGTTCACCAAGTATGGTTTATGACAACTATAAA
 GCTACAGCAGGTAAAGAAAGAGCTTTATATTGTAAAGGGGCAAAACATGC
 GAAATCTTTTGAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTT
 TTTTGA AAAAATATGAAAAA

SEQ ID NO. 8303

STRAIN A909

AATCCTTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTTATATGCT
 TATGATAAATCCTTTGATAAGCTATTAAAGCAAAAATAGAAATGACAAA
 CCAAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGCTAAGAAAACTC
 ATAAGACAGCTGTTGTCGTTTCATGGTTTTGCGAATAGCAAAGAGAATATG
 AAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTCTTATGCC
 TGACAAACATGACATGGTGAAAGTCATGGGCAGTTGATAGGCTATGGCT
 GGAACGACCGCGAAGCAATTTCAATGGACAGAAATGATAGTTGATAAG
 AATTCTCAAGCCAAATTACTTTATTGGTGTTCATGGGTGGAGCAAC
 AGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTTAATATCA
 TTGAAGATGCGGTTATTCTGGTGTTCGGGATGAATTAATTTTACAGGCT
 AAAGAGATGTATGGTTTACCAGCCTTCCCCTCTTATATGAAGTTTCAAC
 AATTTCTAAATCAGAGCAGGTTTTCTGTATGGACAAGCAAGTAGTGTGCG
 AACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCATGGTGATAAG
 GATAATTTTGTTCACCAAGTATGGTTTATGACAACTATAAGCTACAGC
 AGGTAAGAAAGAGCTTTATATTGTAAAGGGGCAAAACATGCGAAATCTT
 TTGAAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTTTTTGAAA
 AAATATGAAAAA

SEQ ID NO. 8304

STRAIN H36B

AGTTTTTATTTTTTCCACGTTGCCCAAGTTTCGAGATGATAAATCCTTTAT
 TTCAAATGGTCAACGTAAGCCTGGAAACTCTTTATATGCTTATGATAAAT
 CCTTTGATAAGCTATTAAAGCAAAAATAGAAATGACAAACCAAAATATA
 AAGCAAGTTGCTTGGTATGTTCTGCTGCTAAGAAAACTCATAAGACAGC
 TGTGTCTGTTTCATGGTTTTGCGAATAGCAAAGAGAATATGAAGGCATATG
 GTTGGCTGTTTCATAAGTTAGGATACAATGTTCTTATGCTTGACAACATT
 GCACATGGTGAAAGTCATGGGCAGTTGATAGGCTATGGCTGGAACGACCG
 CGAGAACATTATCAATGGACAGAAATGATAGTTGATAAGAAATTCATCAA
 GCCAAATTACTTTATTGGTGTTCATGGGTGGAGCAACAGTCATGATG
 GCTAGTGGTGAAAAATTACCTAGTCAGGTTGTTAATATCATTGAAGATTG
 CGGTTATTCTGGTGTTCGGGATGAATTAATTTTACAGGCTAAAGAGATGT
 ATGGTTTACCAGCCTTCCCCTCTTATATGAAGTTTCAACAATTTCTAAA
 ATCAGAGCAGGTTTTCTGTATGGACAAGCAAGTAGTGTGCAACAAATTGAA
 AAAGAATAATTTACCAGCCCTCTTTATTTCATGGTGATAAGGATAATTTTG
 TTCCAACAAGTATGGTTTATGACAACTATAAGCTACAGCAGGTAAGAAA
 GAGCTTTATATTGTAAAGGGGCAAAACATGCGAAATCTTTTGAACAGA
 GCCAGAAAAATATGAGAAACGTATCTCTAGTTTTTTGAAAAAATATGAAA
 AA

SEQ ID NO. 8305

STRAIN 18RS21

Table 83: Comparative Sequences relating to SAG0108

GCTAGTTTTATTTTTTCCACGTTGCCCAAGTTCGA
 GATGATAAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAACTCTTT
 ATATGCTTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAA
 TGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTCTGCTGTTAAG
 AAAACTCATAAGACAGCTGTGTGCTTCATGGTTTTCGGAATAGCAAAAGA
 GAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTTC
 TTATGCTTGACAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGC
 TATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
 TGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTG
 GAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTT
 AATATCATTGAAGATTGCGGTTATTCTAGTGTGGGATGAATTAAAAAT
 TCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAG
 TTTCAACAATTTCTAAAATCAGAGCAGGTTTTCGTATGGACAAGCAAGT
 AGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCTATGG
 TGATAAGGATAAATTTGTTCCAACAAGTATGGTTTATGACAACTATAAAG
 CTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGCG
 AAATCTTTTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTT
 TTTGAAAAAATATGAAAAA

SEQ ID NO. 8306

STRAIN M732

GCTAGTTTTATTTTTTCCACGTTGCCCAAGTTCGA
 GATGATAAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAACTCTTT
 ATATGCTTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAA
 TGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTCTGCTGCTAAG
 AAAACTCATAAGACAGTTGTGTGCTTCATGGTTTTCGGAATAGCAAAAGA
 GAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTTC
 TTATGCTTGACAACATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGC
 TATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
 GGATAAGAATCCATCAAGCCAAATTaCTTTATTTGGTGTTCATGGGTG
 GAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTT
 AATATCATTGAAGATTGTGGTTATTCTAGTGTGGGATGAATTAAAAAT
 TCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAG
 TTTCAACAATTTCTAAAATCAGAGCAGGTTTTCGTATGGACAAGCAAGT
 AGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCTATGG
 TGATAAGGATAAATTTGTTCCAACAAGTATGGTTTATGACAACTATAAAG
 CTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGCG
 AAATCTTTTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTT
 TTTGAAAAAATATGAAAAA

SEQ ID NO. 8307

STRAIN COH1

GCTAGTTTTATTTTTTCCACGTTGCCCAAGTTCG
 GAGATGATAAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAACTCT
 TTATATGCTTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAA
 AATGaCAAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTCTGCTGCTA
 AGAAAACTCATAAGACAGTTGTGTGCTTCATGGTTTTCGGAATAGCAAAA
 GAGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGT
 TCTTATGCTTGACAACATTGCACATGGTGAAAGTCATGGGCAGTTGATAG
 CTATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATA
 GTGGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTG
 TGGAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTG
 TTAATATCATTGAAGATTGTGGTTATTCTAGTGTGGGATGAATTAAAA
 TTTCAAGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGA
 AGTTTCAACAATTTCTAAAATCAGAGCAGGTTTTCGTATGGACAAGCAA
 GTAGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCTAT
 GGTGATAAGGATAAATTTGTTCCAACAAGTATGGTTTATGACAACTATAA
 AGCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATG
 CGAAATCTTTTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGT
 TTTTGAAAAAATATGAAAAA

SEQ ID NO. 8308

STRAIN M781

GCTAGTTTTATTTTTTCCACGTTGCCCAAGTTCG
 AGATGATAAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAACTCTT
 TATATGCTTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAA
 ATGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTCTGCTGCTAA
 GAAAACTCATAAGACAGTTGTGTGCTTCATGGTTTTCGGAATAGCAAAAG
 AGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTT
 CTTATGCTTGACAACATTGCACATGGTGAAAGTCATGGGCAGTTGATAGG
 CTATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAG
 TGGATAAGAATCCATCAAGCCAAATTaCTTTATTTGGTGTTCATGGGTG
 GGAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTT
 TAAATATCATTGAAGATTGTGGTTATTCTAGTGTGGGATGAATTAAAA
 TTCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGA
 GTTTCAACAATTTCTAAAATCAGAGCAGGTTTTCGTATGGACAAGCAAG
 TAgTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCTATG
 GTGATAAGGATAAATTTGTTCCAACAAGTATGGTTTATGACAACCTATAA
 GCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATG
 GAAATCTTTTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGT
 TTTTGAAAAAATATGAAAAA

SEQ ID NO. 8309

Table 83: Comparative Sequences relating to SAG0108

STRAIN CJB110

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCGAG
 ATGATAAATCCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTTA
 TATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAAT
 GACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGCTAAGA
 AAACCTATAAGACAGCTGTTGCTGTTTCATGGTTTTGCGAATAGCAAAGAG
 AATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTCT
 TATGCTGTGACAAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGCT
 ATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGTT
 GATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTGG
 AGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTTA
 ATATCATTGAAGATTGCGGTTATTCTAGTGTTTGGGATGAATTAATAATTT
 CAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAGT
 TTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGTA
 GTGTGGAACAATTGAAAAAGAAATAATTACCAGCCCTCTTTATTCATGGT
 GATAAGGATAAATTTGTTCCAACAAGTATGGTTTATGACAACTATAAAGC
 TACAGCAGGTAAGAAAGAGCTTTATATTTGTAAGGGGGCAAAACATGCGA
 AATCTTTTGAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTTT
 TTGAAAAAATATGAAAAA

SEQ ID NO. 8310

STRAIN 1169NT

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCGA
 GATGATAAATCCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTT
 ATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAA
 TGACAAACCcAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGCTAAG
 AAAACCTATAAGACAGCTGTTGCTGTTTCATGGTTTTGCGAATAGCAAAGA
 GAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTCT
 TTATACCTGACAAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGC
 TATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
 TGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTGG
 GAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTT
 AATATCATTGAAGATTGCGGTTATTCTAGTGTTTGGGATGAATTAATAAT
 TCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAG
 TTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGT
 AGTGTAGAACAAATTGAAAAAGAAATAATTACCAGCCCTCTTTATTCATGG
 TGATAAGGATAAATTTGTTCCAACAAGTATGGTTTATGACAACTATAAAG
 CTACAGCAGGTAAGAAAGAGCTTTATATTTGTAAGGGGGCAAAACATGCG
 AATCTTTTGAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTTT
 TTTGAAAAAATATGAAAAA

SEQ ID NO. 8311

STRAIN JM9130013

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCG
 AGATGATAAATCCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTT
 TATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAA
 ATGaCAAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGTTAA
 GAAAACTCATAAGACAGCTGTTGCTGTTTCATGGTTTTGCGAATAGCAAAG
 AGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTT
 CTATGCTGACAAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGG
 CTATGGCTGGAACGACCGCGAGAACATTATCaAATGGACAGAAATGATAG
 TTGATAAGAATCCATCAAGCCAAATTaCTTTATTTGGTGTTCATGGGT
 GGAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGT
 TAATATCATTGAAGATTGCGGTTATTCTAGTGTTTGGGATGAATTAATAAT
 TTCAAGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAG
 GTTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAG
 TAGTGTGGAACAATTGAAAAAGAAATAATTACCAGCCCTCTTTATTCATG
 GTGATAAGGATAAATTTGTTCCAACAAGTATGGTTTATGACAACTATAAAG
 GCTACAGCAGGTAAGAAAGAGCTTTATATTTGTAAGGGGGCAAAACATGCG
 GAAATCTTTTGAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTT
 TTTTGAAAAAATATGAAAAA

PRETTY of: /biotmp/msa286608.2{*} February 24, 2003 06:26 ..

	1				50
msa286608.2{662_COH1}	-----	-----	-----	-----	-----
msa286608.2{662_M732}	-----	-----	-----	-----	-----
msa286608.2{662_M781}	-----	-----	-----	-----	-----
msa286608.2{662_A909}	-----	-----	-----	-----	-----
msa286608.2{662_H36B}	-----	-----	-----	-----	-----
msa286608.2{662_090}	-----	-----	-----	-----	-----
msa286608.2{662_CJB110}	-----	-----	-----	-----	-----
msa286608.2{662_18RS21}	-----	-----	-----	-----	-----
msa286608.2{662_2603}	atgaaaaaga	ttcgattatc	aaagtttatt	aaaatgattg	ttgtattttt
msa286608.2{662_JM9130013}	-----	-----	-----	-----	-----
msa286608.2{662_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****

	51				100
msa286608.2{662_COH1}	-----g	ctagttttta	ttttttccac	gttgcccaag	
msa286608.2{662_M732}	-----g	ctagttttta	ttttttccac	gttgcccaag	
msa286608.2{662_M781}	-----g	ctagttttta	ttttttccac	gttgcccaag	

Table 83: Comparative Sequences relating to SAG0108

msa286608.2{662_A909}	-----	-----	-----	-----	-----
msa286608.2{662_H36B}	-----	-----	--agtttttta	ttttttccac	gttgcccaag
msa286608.2{662_090}	-----	-----	ctagtttttta	ttttttccac	gttgcccaag
msa286608.2{662_CJB110}	-----	-----	ctagtttttta	ttttttccac	gttgcccaag
msa286608.2{662_18RS21}	-----	-----	ctagtttttta	ttttttccac	gttgcccaag
msa286608.2{662_2603}	gtttttaatt	agtgttagcag	ctagtttttta	ttttttccac	gttgcccaag
msa286608.2{662_JM9130013}	-----	-----	ctagtttttta	ttttttccac	gttgcccaag
msa286608.2{662_1169NT}	-----	-----	ctagtttttta	ttttttccac	gttgcccaag
Consensus	*****	*****	-----	-----	-----
101					
msa286608.2{662_COH1}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCACGTAA	GCCTGGAAAC
msa286608.2{662_M732}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCACGTAA	GCCTGGAAAC
msa286608.2{662_M781}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCACGTAA	GCCTGGAAAC
msa286608.2{662_A909}	-----	--AATCCTTT	ATTTCAAATG	GTCACGTAA	GCCTGGAAAC
msa286608.2{662_H36B}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCACGTAA	GCCTGGAAAC
msa286608.2{662_090}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCACGTAA	GCCTGGAAAC
msa286608.2{662_CJB110}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCACGTAA	GCCTGGAAAC
msa286608.2{662_18RS21}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCACGTAA	GCCTGGAAAC
msa286608.2{662_2603}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCACGTAA	GCCTGGAAAC
msa286608.2{662_JM9130013}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCACGTAA	GCCTGGAAAC
msa286608.2{662_1169NT}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCACGTAA	GCCTGGAAAC
Consensus	-----	*****	*****	*****	*****
151					
msa286608.2{662_COH1}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_M732}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_M781}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_A909}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_H36B}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_090}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_CJB110}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_18RS21}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_2603}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_JM9130013}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_1169NT}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
Consensus	*****	*****	*****	*****	*****
201					
msa286608.2{662_COH1}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_M732}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_M781}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_A909}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_H36B}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_090}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_CJB110}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_18RS21}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_2603}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_JM9130013}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_1169NT}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
Consensus	*****	*****	*****	*****	*****
251					
msa286608.2{662_COH1}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_M732}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_M781}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_A909}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_H36B}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_090}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_CJB110}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_18RS21}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_2603}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_JM9130013}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_1169NT}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
Consensus	*****	*****	*****	*****	*****
301					
msa286608.2{662_COH1}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_M732}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_M781}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_A909}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_H36B}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_090}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_CJB110}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_18RS21}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_2603}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_JM9130013}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_1169NT}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
Consensus	*****	*****	*****	*****	*****
351					
msa286608.2{662_COH1}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_M732}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
400					

Table 83: Comparative Sequences relating to SAG0108

msa286608.2{662_M781}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_A909}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_H36B}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_090}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_CJB110}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_18RS21}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_2603}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_JM9130013}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_1169NT}	TGTTCTTATa	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
Consensus	*****-*	*****-*	*****	*****	*****
msa286608.2{662_COH1}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_M732}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_M781}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_A909}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_H36B}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_090}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_CJB110}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_18RS21}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_2603}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_JM9130013}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_1169NT}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	ATAGTgGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTtTG	GTGTTTCAAT
msa286608.2{662_M732}	ATAGTgGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTtTG	GTGTTTCAAT
msa286608.2{662_M781}	ATAGTgGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTtTG	GTGTTTCAAT
msa286608.2{662_A909}	ATAGTtGATA	AGAATtCATC	AAGCCAAATT	ACTTTATTtTG	GTGTTTCAAT
msa286608.2{662_H36B}	ATAGTtGATA	AGAATtCATC	AAGCCAAATT	ACTTTATTtTG	GTGTTTCAAT
msa286608.2{662_090}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTtTG	GTGTTTCAAT
msa286608.2{662_CJB110}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTtTG	GTGTTTCAAT
msa286608.2{662_18RS21}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTtTG	GTGTTTCAAT
msa286608.2{662_2603}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTtTG	GTGTTTCAAT
msa286608.2{662_JM9130013}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTtTG	GTGTTTCAAT
msa286608.2{662_1169NT}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTtTG	GTGTTTCAAT
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_M732}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_M781}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_A909}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_H36B}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_090}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_CJB110}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_18RS21}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_2603}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_JM9130013}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_1169NT}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_M732}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_M781}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_A909}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTgGTGTTTg	GGATGAATTA
msa286608.2{662_H36B}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTgGTGTTTg	GGATGAATTA
msa286608.2{662_090}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_CJB110}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_18RS21}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_2603}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_JM9130013}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_1169NT}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
Consensus	*****	*****	**..*****	**..*****	*****
msa286608.2{662_COH1}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTtTATA
msa286608.2{662_M732}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTtTATA
msa286608.2{662_M781}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTtTATA
msa286608.2{662_A909}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTtTATA
msa286608.2{662_H36B}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTtTATA
msa286608.2{662_090}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTtTATA
msa286608.2{662_CJB110}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTtTATA
msa286608.2{662_18RS21}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTtTATA
msa286608.2{662_2603}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTtTATA
msa286608.2{662_JM9130013}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTtTATA
msa286608.2{662_1169NT}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTtTATA
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTtTCG	TATGGACAAG

Table 83: Comparative Sequences relating to SAG0108

msa286608.2{662_M732}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_M781}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_A909}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_H36B}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_090}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_CJB110}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_18RS21}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_2603}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_JM9130013}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_1169NT}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_M732}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_M781}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_A909}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_H36B}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_090}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_CJB110}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_18RS21}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_2603}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_JM9130013}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_1169NT}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_M732}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_M781}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_A909}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_H36B}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_090}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_CJB110}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_18RS21}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_2603}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_JM9130013}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_1169NT}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_M732}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_M781}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_A909}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_H36B}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_090}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_CJB110}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_18RS21}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_2603}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_JM9130013}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_1169NT}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	ATGCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_M732}	ATGCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_M781}	ATGCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_A909}	ATGCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_H36B}	ATGCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_090}	ATGCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_CJB110}	ATGCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_18RS21}	ATGCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_2603}	ATGCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_JM9130013}	ATGCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_1169NT}	ATGCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_M732}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_M781}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_A909}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_H36B}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_090}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_CJB110}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_18RS21}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_2603}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_JM9130013}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_1169NT}	AGTTTTTTGA	AAAAATATGA	AAAA		
Consensus	*****	*****	*****		

SEQ ID NO. 8312

Table 83: Comparative Sequences relating to SAG0108

STRAIN 2603 frame: 1

MKKIRLSKFIKMIIVILFLISVAASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFD
KLLKQKIEMTNQNIKQVAVYVPAVKKTKHTAVVVHGFANSKENMKAYGWLPHKLGYNVLM
PDNIAHGESHGQLIGYGWNDRENI IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKL
PSQVVNI IEDCGYSSVWDELKFKQAKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQL
KKNLPALEFIHGDKDNFVPTSMVYDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRIS
SFLKKYEK

SEQ ID NO. 8313

STRAIN 090 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
AKKTHKTAVVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
I IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNLPALEFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISFLKKYEK

SEQ ID NO. 8314

STRAIN A909 frame: 3

SFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPAKKTHKTAVVVHGF
NSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYGWNDRENI IKWTEMIVDKNSS
QITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQAKEMYGLPAFPLLYE
VSTISKIRAGFSYGQASSVEQLKKNLPALEFIHGDKDNFVPTSMVYDNYKATAGKKELYI
VKGAKHAKSFETEPEKYEKRISFLKKYEK

SEQ ID NO. 8315

STRAIN H36B frame: 1

SFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
KKTHKTAVVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
I IKWTEMIVDKNSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNLPALEFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISFLKKYEK

SEQ ID NO. 8316

STRAIN 18RS21 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
VKTHKTAVVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
I IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNLPALEFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISFLKKYEK

SEQ ID NO. 8317

STRAIN M732 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
AKKTHKTAVVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
I IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNLPALEFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISFLKKYEK

SEQ ID NO. 8318

STRAIN COH1 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
AKKTHKTAVVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
I IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNLPALEFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISFLKKYEK

SEQ ID NO. 8319

STRAIN M781 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
AKKTHKTAVVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
I IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNLPALEFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISFLKKYEK

SEQ ID NO. 8320

STRAIN CJB110 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
AKKTHKTAVVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
I IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNLPALEFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISFLKKYEK

SEQ ID NO. 8321

STRAIN 1169NT frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
AKKTHKTAVVVHGFANSKENMKAYGWLPHKLGYNVLI PDNIAHGESHGQLIGYGWNDREN
I IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNLPALEFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISFLKKYEK

SEQ ID NO. 8322

Table 83: Comparative Sequences relating to SAG0108

STRAIN JM9130013 frame: 1

ASFFYFFHVAQVRDDKSF ISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
 VKKTHKTAVVVHGFANSKENMKAYGWL FHLGYNVLPDNIHAGESHGQLIGYGWDRN
 IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPQVNNIIEDCGYSSVWDELKFO
 AKEMYGLPAFPLLYEVSTISKIRAGFSYQASSVEQLKKNLPALEFIHGDKNFVPTSMV
 YDNYKATAGKELYIVGAKHAKSFETEPEKYEKRISFLKKEK

PRETTY of: /biotmp/msa286876.2{*} February 24, 2003 06:46 ..

	1				50
msa286876.2{662_A909}	-----	-----	-----	-----SF	ISNGQRKPGN
msa286876.2{662_H36B}	-----	-----	-----SFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_COH1}	-----	-----	-----ASFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_M732}	-----	-----	-----ASFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_M781}	-----	-----	-----ASFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_18RS21}	-----	-----	-----ASFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_2603}	mkkirlskfi	kmivvilfli	svaASFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_JM9130013}	-----	-----	-----ASFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_090}	-----	-----	-----ASFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_CJB110}	-----	-----	-----ASFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_1169NT}	-----	-----	-----ASFYFFH	VAQVRDDKSF	ISNGQRKPGN
Consensus	*****	*****	*****	*****	*****
	51				100
msa286876.2{662_A909}	SLYAYDKSFD	KLLKQKIEMT	NONIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_H36B}	SLYAYDKSFD	KLLKQKIEMT	NONIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_COH1}	SLYAYDKSFD	KLLKQKIEMT	NONIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_M732}	SLYAYDKSFD	KLLKQKIEMT	NONIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_M781}	SLYAYDKSFD	KLLKQKIEMT	NONIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_18RS21}	SLYAYDKSFD	KLLKQKIEMT	NONIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_2603}	SLYAYDKSFD	KLLKQKIEMT	NONIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_JM9130013}	SLYAYDKSFD	KLLKQKIEMT	NONIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_090}	SLYAYDKSFD	KLLKQKIEMT	NONIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_CJB110}	SLYAYDKSFD	KLLKQKIEMT	NONIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_1169NT}	SLYAYDKSFD	KLLKQKIEMT	NONIKQVAVY	VPAaKKTHTK	avVVHGFANS
Consensus	*****	*****	*****	*****	*****
	101				150
msa286876.2{662_A909}	KENMKAYGWL	FHLGYNVLM	PDNIHAGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_H36B}	KENMKAYGWL	FHLGYNVLM	PDNIHAGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_COH1}	KENMKAYGWL	FHLGYNVLM	PDNIHAGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_M732}	KENMKAYGWL	FHLGYNVLM	PDNIHAGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_M781}	KENMKAYGWL	FHLGYNVLM	PDNIHAGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_18RS21}	KENMKAYGWL	FHLGYNVLM	PDNIHAGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_2603}	KENMKAYGWL	FHLGYNVLM	PDNIHAGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_JM9130013}	KENMKAYGWL	FHLGYNVLM	PDNIHAGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_090}	KENMKAYGWL	FHLGYNVLM	PDNIHAGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_CJB110}	KENMKAYGWL	FHLGYNVLM	PDNIHAGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_1169NT}	KENMKAYGWL	FHLGYNVLM	PDNIHAGESH	GQLIGYGWND	RENI IKWTEM
Consensus	*****	*****	*****	*****	*****
	151				200
msa286876.2{662_A909}	IVDKNsSSQI	TLFGVSMGGA	TVMASGEKL	PSQVNNIIED	CGYSgVWDEL
msa286876.2{662_H36B}	IVDKNsSSQI	TLFGVSMGGA	TVMASGEKL	PSQVNNIIED	CGYSgVWDEL
msa286876.2{662_COH1}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVNNIIED	CGYSsVWDEL
msa286876.2{662_M732}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVNNIIED	CGYSsVWDEL
msa286876.2{662_M781}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVNNIIED	CGYSsVWDEL
msa286876.2{662_18RS21}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVNNIIED	CGYSsVWDEL
msa286876.2{662_2603}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVNNIIED	CGYSsVWDEL
msa286876.2{662_JM9130013}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVNNIIED	CGYSsVWDEL
msa286876.2{662_090}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVNNIIED	CGYSsVWDEL
msa286876.2{662_CJB110}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVNNIIED	CGYSsVWDEL
msa286876.2{662_1169NT}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVNNIIED	CGYSsVWDEL
Consensus	*****	*****	*****	*****	*****
	201				250
msa286876.2{662_A909}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEFI
msa286876.2{662_H36B}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEFI
msa286876.2{662_COH1}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEFI
msa286876.2{662_M732}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEFI
msa286876.2{662_M781}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEFI
msa286876.2{662_18RS21}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEFI
msa286876.2{662_2603}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEFI
msa286876.2{662_JM9130013}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEFI
msa286876.2{662_090}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEFI
msa286876.2{662_CJB110}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEFI
msa286876.2{662_1169NT}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEFI
Consensus	*****	*****	*****	*****	*****
	251				300
msa286876.2{662_A909}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_H36B}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_COH1}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS

Table 83: Comparative Sequences relating to SAG0108

msa286876.2{662_M732}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_M781}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_18RS21}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_2603}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_JM9130013}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_090}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_CJB110}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_1169NT}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
Consensus	*****	*****	*****	*****	*****
301					
msa286876.2{662_A909}	SFLKKYEK				
msa286876.2{662_H36B}	SFLKKYEK				
msa286876.2{662_COH1}	SFLKKYEK				
msa286876.2{662_M732}	SFLKKYEK				
msa286876.2{662_M781}	SFLKKYEK				
msa286876.2{662_18RS21}	SFLKKYEK				
msa286876.2{662_2603}	SFLKKYEK				
msa286876.2{662_JM9130013}	SFLKKYEK				
msa286876.2{662_090}	SFLKKYEK				
msa286876.2{662_CJB110}	SFLKKYEK				
msa286876.2{662_1169NT}	SFLKKYEK				
Consensus	*****				

Table 84: Comparative Sequences relating to SAG0267

SEQ ID NO. 8401

STRAIN 2603

ATGATGAAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCAGTGGCTGTACTAAAC
 AATATGGAATGTTTAGCGACTGTCACTATCAATATCAAAAAGAAATCATAGCATTAAATTTG
 ATGCCAGCCATTGATTTTAAATGCAATCAATTGATTAGAACCTCAAGATTGGACCGT
 ATCGTAGTAGCAGAGGGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGTACAGCA
 AAAATGCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACGCTTTA
 ACAAATGGATTTTCAGAAAATGATTTATTTGGTACCCTTATAGATGCACGACGTAATAAT
 GTTTATGTTGTTTCTATCAAAATGGTGATACTGTTAAACCAGACTGTACACTTCTCTT
 GAAGAAGTCTTACAAGAGGTGGGAATAAAGCCAATGTTTATTGTCGGAGAGGTTGCA
 GCATTTTGTGATCAGATTAAAGAAAGCCTTACCACATGCTAAAATTACAGAAACCTTTACCT
 TGTGCAGTAGCAATTGGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATGCGTTT
 GTTCCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTAAAAAACCACTGTGAA
 ACGAATACAGAAGATATATTAAAGAGAGTT

SEQ ID NO. 8402

STRAIN 090

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCAGTGGCTGTACT
 AAAAATATGGAATGTTTAGCGACTGTCACTATCAATATCAAAAAGAAATC
 ATAGCATTAAATTTGATGCCAGCCATTGATTTTAAATGCAATCAATTGAT
 TTAGAACCTCAAGATTGGAGCCGATCGTAGTGGCAGAGGGTCCAGGATC
 TTATACGGGCTTACGTGTAGCTGTTGTACAGCAAAAATGCTAGCTTATA
 CGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACGCTTTAAACAAAT
 GGATTTTCAGAAAATGATTTGTTGGTACCCTTATAGATGCACGACGTAA
 CAATGTTTATGTTGTTTCTATCAAAATGGTGATACTGTTAAACCAGACT
 GTACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGAATAAAGCCAAT
 GTTCATTTTGTGGAGAGGTTGCAGCATTTTGTGATCAGATTAAAGAAAGC
 CTTACCACATGCTAAAATTACAGAAACCTTTACCTTGTGCAGTGGCAATTG
 GCGCAAGAGGACAAAAATGGAAGCGTTAATGTAGATGCGTTTGTTCAC
 CGATACTTAAACAGAGTTGAAGCTGAGGAAAATTGGTTAAAAAACCACTG
 TGAACGAAT

SEQ ID NO. 8403

STRAIN A909

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCAG
 TGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATATC
 AAAAAAGAAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTAAATGCA
 ATCAATTGATTAGAACCTCAAGATTGGACCGTATCGTAGTAGCAGAGG
 GTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGTCTACAGCAAAAATG
 CTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACGC
 TTTAAACAAATGGATTTTCAGAAAATGATTTATTTGGTACCCTTATAGATG
 CACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGTT
 AAACCAGACTGTCACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGAA
 TAAAGCCAATGTTTATTTGTTCGGAGAGGTTGCAGCATTTGTTGACCAGA
 TTAAGAAAGTTTACCACATGCTAAAATTACAGAACTTTACCTTGTGCA
 GCGGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATGC
 GTTTGTTCCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTAA
 GAAACCACTGTGAACGAAT

SEQ ID NO. 8404

STRAIN H36B

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAAGAAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTAAATGC
 AATCAATTGATTAGAACCTCAAGATTGGACCGTATCGTAGTAGCAGAG
 GGTCAGGATCTTATACGGGCTTACGTGTAGCTGTTGTCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAAACAAATGGATTTTCAGAAAATGATTTATTTGGTACCCTTATAGAT
 GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGT
 TAAACAGACTGTCACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTTATTTGTTCGGAGAGGTTGCAGCATTTGTTGACCAG
 ATTAAGAAAGTTTACCACATGCTAAAATTACAGAACTTTACCTTGTGCA
 AGTGGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATG
 CGTTTGTTCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTA
 AGAAACCACTGTGAACGAATACAGAAGATATATTAAAGAGAGTT

SEQ ID NO. 8405

STRAIN 18RS21

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAAGAAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTAAATGC
 AATCAATTGATTAGAACCTCAAGATTGGACCGTATCGTAGTAGCAGAG
 GGTCAGGATCTTATACGGGCTTACGTGTAGCTGTTGTCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAAACAAATGGATTTTCAGAAAATGATTTATTTGGTACCCTTATAGAT
 GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGT
 TAAACAGACTGTCACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTTATTTGTTCGGAGAGGTTGCAGCATTTTGTGACCAG
 ATTAAGAAAGTTTACCACATGCTAAAATTACAGAACTTTACCTTGTGCA
 AGTGGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATG
 CGTTTGTTCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTA
 AGAAACCACTGTGAACGAATACAGAAGATATATTAAAGAGAGTT

Table 84: Comparative Sequences relating to SAG0267

SEQ ID NO. 8406

STRAIN M732

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAATGC
 AATCAATTGATTAGAACCTCAAGATTGGACCGTATCGTAGTAGCAGAG
 GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAAACAAATGGATTTCAGAAAATGATTTATTGGTACCACCTTATAGAT
 GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGACTGT
 TAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTTCATTTTGTGCGAGAGGTTGCAGCATTTTTTGATCAG
 ATTAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCTTGTGC
 AGTAGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGAnn
 CGTTTGTTCACGATACCTTAAACGTTGTTGAAGCTGAGGAAAATTGGTTA
 AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

SEQ ID NO. 8407

STRAIN COH1

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCAC
 TATCAGTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATC
 AATATCAAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTT
 AATGCAATCAATTGATTAGAACCTCAAGATTGGACCGTATCGTAGTAG
 CAGAGGGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCA
 AAAATGCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCT
 GTACGCTTTAAACAAATGGATTTCAGAAAATGATTTATTGGTACCACCTTA
 TAGATGCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGAT
 ACTGTTAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGT
 GGGGAATAAAGCCAATGTTTCATTTTGTGCGAGAGGTTGCAGCATTTTTTG
 ATCAGATTAAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCT
 TGTGCAGTAGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGT
 AGATGCGTTTGTTCACGATACCTTAAACGTTGTTGAAGCTGAGGAAAATT
 GGTAAAAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

SEQ ID NO. 8408

STRAIN M781

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTA
 TCAGTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAA
 TATCAAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAA
 TGCAATCAATTGATTAGAACCTCAAGATTGGACCGTATCGTAGTAGTCA
 GAGGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAA
 AATGCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGT
 ACGCTTTAAACAAATGGATTTCAGAAAATGATTTATTGGTACCACCTTATA
 GATGCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGATA
 TGTTAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGG
 GGAATAAAGCCAATGTTTCATTTTGTGCGAGAGGTTGCAGCATTTTTTGAT
 CAGATTAAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCTTG
 TGCAGTAGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAG
 ATGCGTTTGTTCACGATACCTTAAACGTTGTTGAAGCTGAGGAAAATTGG
 TAAAAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

SEQ ID NO. 8409

STRAIN CJB110

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAATGC
 AATCAATTGATTAGAACCTCAAGATTGGACCGTATCGTAGTGCCAGAG
 GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAAACAAATGGATTTCAGAAAATGATTTGTTGGTACCACCTTATAGAT
 GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGACTGT
 TAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTTCATTTTGTGCGAGAGGTTGCAGCATTTTTTgATCAG
 ATTAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCTTGTGC
 AGTGGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATG
 CGTTTGTTCACGATACCTTAAACGAGTTGAAGCTGAGGAAAATTGGTTA
 AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

SEQ ID NO. 8410

STRAIN I169NT

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAATGC
 AATCAATTGATTAGAACCTCAAGATTGGACCGTATCGTAGTAGCAGAG
 GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAAACAAATGGATTTCAGAAAATGATTTATTGGTACCACCTTATAGAT
 GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGACTGT
 TAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTTCATTTTGTGCGAGAGGTTGCAGCATTTTTTgATCAG
 ATTAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCTTGTGC
 AGTGGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATG
 CGTTTGTTCACGATACCTTAAACGAGTTGAAGCTGAGGAAAATTGGTTA
 AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

Table 84: Comparative Sequences relating to SAG0267

AGTGGCAATTGGGCGCAAAGGACAAAAATGGAAGCGTTAATGTAGATG
CGTTTGTTCACGATACCTTAAACGTGTTGAAGCTGAGGAAATTTGGTTA
AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

SEQ ID NO.: 8411

STRAIN JM9130013

AAAGTTTTAGCCTTTGATACCTTCAAGCAAAGCACTATCA
GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
CAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTAATGC
AATCAATTGATTAGAACCTCAAGATTGGACCGTATCGTAGTAGCAGAG
GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAT
gCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
CTTTAACAAATGGATTTCAGAAAATGATTTATTGGTACCCTTATAGAT
GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGT
TAAACCACTGTCACTTCTCTTGAAGAAGCTTACAAGAGGTGGGGA
ATAAAGCCAATGTTTCATTTTGTGCGAGAGGTTGCAGCATTGTTGACCAG
ATTAAGAAAGTTTACCACATGCTAAAATTACAGAACTTTACCTTGTGC
AGTGGCAATTGGGCGCAAAGGACAAAAATGAAAGCGTTAATGTAGATG
CGTTTGTTCACGATACCTTAAACGTGTTGAAGCTGAGGAAATTTGGTTA
AGAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

PRETTY of: /biotmp/msa521675.2{*} March 10, 2003 08:34 ..

	1		50
msa521675.2{69_A909}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_H36B}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_JM9130013}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_1169NT}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_090}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_CJB110}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_18RS21}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_2603}	atgatgAAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_COH1}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_M732}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_M781}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
Consensus	*****	*****	*****

	51		100
msa521675.2{69_A909}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_H36B}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_JM9130013}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_1169NT}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_090}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_CJB110}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_18RS21}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_2603}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_COH1}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_M732}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_M781}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
Consensus	*****	*****	*****

	101		150
msa521675.2{69_A909}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_H36B}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_JM9130013}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_1169NT}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_090}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_CJB110}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_18RS21}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_2603}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_COH1}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_M732}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_M781}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
Consensus	*****	*****	*****

	151		200
msa521675.2{69_A909}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_H36B}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_JM9130013}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_1169NT}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_090}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_CJB110}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_18RS21}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_2603}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_COH1}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_M732}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_M781}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
Consensus	*****	*****	*****

	201		250
msa521675.2{69_A909}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT TGCTACAGCA AAAATGCTAG
msa521675.2{69_H36B}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT TGCTACAGCA AAAATGCTAG

Table 84: Comparative Sequences relating to SAG0267

msa521675.2{69_JM9130013}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
msa521675.2{69_1169NT}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
msa521675.2{69_090}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
msa521675.2{69_CJB110}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
msa521675.2{69_18RS21}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
msa521675.2{69_2603}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
msa521675.2{69_COH1}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
msa521675.2{69_M732}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
msa521675.2{69_M781}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
Consensus	*****	*****	*****	*****	*****
251					
msa521675.2{69_A909}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_H36B}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_JM9130013}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_1169NT}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_090}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_CJB110}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_18RS21}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_2603}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_COH1}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_M732}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_M781}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
Consensus	*****	*****	*****	*****	*****
301					
msa521675.2{69_A909}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_H36B}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_JM9130013}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_1169NT}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_090}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_CJB110}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_18RS21}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_2603}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_COH1}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_M732}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_M781}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
Consensus	*****	*****	*****	*****	*****
351					
msa521675.2{69_A909}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGaGAT	ACTGTTAAAC
msa521675.2{69_H36B}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGaGAT	ACTGTTAAAC
msa521675.2{69_JM9130013}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGaGAT	ACTGTTAAAC
msa521675.2{69_1169NT}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_090}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_CJB110}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_18RS21}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_2603}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_COH1}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_M732}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_M781}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
Consensus	*****	*****	*****	*****	*****
401					
msa521675.2{69_A909}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_H36B}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_JM9130013}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_1169NT}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_090}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_CJB110}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_18RS21}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_2603}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_COH1}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_M732}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_M781}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
Consensus	*****	*****	*****	*****	*****
451					
msa521675.2{69_A909}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_H36B}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_JM9130013}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_1169NT}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_090}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_CJB110}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_18RS21}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_2603}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_COH1}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_M732}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_M781}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
Consensus	*****	*****	*****	*****	*****
501					
msa521675.2{69_A909}	GAAAGtTTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAgTgG
550					

Table 84: Comparative Sequences relating to SAG0267

msa521675.2{69_H36B}	GAAAGcttTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_JM9130013}	GAAAGcttTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_1169NT}	GAAAGcttTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_090}	GAAAGccTtTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_CJB110}	GAAAGccTtTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_18RS21}	GAAAGccTtTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_2603}	GAAAGccTtTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_COH1}	GAAAGccTtTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_M732}	GAAAGccTtTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_M781}	GAAAGccTtTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
Consensus	*****-***	*****	*****	*****	*****
msa521675.2{69_A909}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_H36B}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_JM9130013}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_1169NT}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_090}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_CJB110}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_18RS21}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_2603}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_COH1}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_M732}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_M781}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
Consensus	*****	*****	*****-***	*****	*****
msa521675.2{69_A909}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAgAAA
msa521675.2{69_H36B}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAgAAA
msa521675.2{69_JM9130013}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAgAAA
msa521675.2{69_1169NT}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_090}	GTTCACGAT	ACTTAAAACG	aGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_CJB110}	GTTCACGAT	ACTTAAAACG	aGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_18RS21}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_2603}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_COH1}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_M732}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_M781}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
Consensus	*****	*****	-*****	*****	*****-***
msa521675.2{69_A909}	CCACTGTGAA	ACGAAT----	-----	-----	690
msa521675.2{69_H36B}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_JM9130013}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_1169NT}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_090}	CCACTGTGAA	ACGAAT----	-----	-----	
msa521675.2{69_CJB110}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_18RS21}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_2603}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_COH1}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_M732}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_M781}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
Consensus	*****	*****	*****	*****	

SEQ ID NO. 8412

STRAIN 2603 frame: 1

MMKVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDR
 IVVAGPGSYTGLRVAVATAKMLAYTLKIDLGVSSLYALTNGFSENDLLVPLIDARRNN
 VYVGFYQNGDTVPKPDCHTSLEEVLQEVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 CAVAIGRKGQKMKSVNVDAFVPRYLKRVEAENWLNHCETNTTEEYIKRV

SEQ ID NO. 8413

STRAIN 090 frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAGPGSYTGLRVAVATAKMLAYTLKIDLGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVPKPDCHTSLEEVLQEVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDAFVPRYLKRVEAENWLNHCETN

SEQ ID NO. 8414

STRAIN A909 frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAGPGSYTGLRVAVATAKMLAYTLKIDLGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVPKPDCHTSLEEVLQEVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDAFVPRYLKRVEAENWLNHCETN

SEQ ID NO. 8415

STRAIN H36B frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAGPGSYTGLRVAVATAKMLAYTLKIDLGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVPKPDCHTSLEEVLQEVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDAFVPRYLKRVEAENWLNHCETNTTEEYIKRV

SEQ ID NO. 8416

Table 84: Comparative Sequences relating to SAG0267

STRAIN 18RS21 frame: 1

KVLAFTSSKALSVAVLNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGIFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQMKMSVNVDAFVPRYLKRVEAENWLKNHCETNTEEYIKRV

SEQ ID NO. 8417

STRAIN M732 frame: 1

KVLAFTSSKALSVAVLNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGIFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQMKMSVNVXXFVPRYLKRVEAENWLKNHCETNTEEYIKRV

SEQ ID NO. 8418

STRAIN COH1 frame: 1

KVLAFTSSKALSVAVLNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGIFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQMKMSVNVDAFVPRYLKRVEAENWLKNHCETNTEEYIKRV

SEQ ID NO. 8419

STRAIN M781 frame: 1

KVLAFTSSKALSVAVLNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VSEGPSTYGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGIFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQMKMSVNVDAFVPRYLKRVEAENWLKNHCETNTEEYIKRV

SEQ ID NO. 8420

STRAIN CJB110 frame: 1

KVLAFTSSKALSVAVLNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGIFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQMKMSVNVDAFVPRYLKRVEAENWLKNHCETNTEEYIKRV

SEQ ID NO. 8421

STRAIN 1169NT frame: 1

KVLAFTSSKALSVAVLNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGIFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQMKMSVNVDAFVPRYLKRVEAENWLKNHCETNTEEYIKRV

SEQ ID NO. 8422

STRAIN JM9130013 frame: 1

KVLAFTSSKALSVAVLNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGIFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQMKMSVNVDAFVPRYLKRVEAENWLKNHCETNTEEYIKRV

PRETTY of: /biotmp/msa521982.2{*} March 10, 2003 08:40 ..

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1                                     50
msa521982.2{69_A909} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_H36B} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_JM9130013} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_090} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_CJB110} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_18RS21} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_2603} mmKVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_COH1} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_M781} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_1169NT} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_M732} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
Consensus *****
51                                     100
msa521982.2{69_A909} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_H36B} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_JM9130013} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_090} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_CJB110} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_18RS21} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_2603} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_COH1} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_M781} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_1169NT} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_M732} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
Consensus *****
101                                     150
msa521982.2{69_A909} TNGFSENDLL VPLIDARRNN VYVGIFYQNGD TVKPDCHTSL EEVLQEVGNK
msa521982.2{69_H36B} TNGFSENDLL VPLIDARRNN VYVGIFYQNGD TVKPDCHTSL EEVLQEVGNK

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Table 84: Comparative Sequences relating to SAG0267

msa521982.2{69_JM9130013}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_090}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_CJB110}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_18RS21}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_2603}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_COH1}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_M781}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_1169NT}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_M732}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
Consensus	*****	*****	*****	*****	*****
151					
msa521982.2{69_A909}	ANVHFVGEVA	AFvDQIKKvL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_H36B}	ANVHFVGEVA	AFvDQIKKvL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_JM9130013}	ANVHFVGEVA	AFvDQIKKvL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_090}	ANVHFVGEVA	AFvDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMeSVNVdaF
msa521982.2{69_CJB110}	ANVHFVGEVA	AFvDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMeSVNVdaF
msa521982.2{69_18RS21}	ANVHFVGEVA	AFvDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_2603}	ANVHFVGEVA	AFvDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_COH1}	ANVHFVGEVA	AFvDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_M781}	ANVHFVGEVA	AFvDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_1169NT}	ANVHFVGEVA	AFvDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMeSVNVdaF
msa521982.2{69_M732}	ANVHFVGEVA	AFvDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVxxF
Consensus	*****	**_*****_*	*****	*****	**_*****_*
201					
msa521982.2{69_A909}	VPRYLKRVEA	EENWLrNHCE	TN-----	230	
msa521982.2{69_H36B}	VPRYLKRVEA	EENWLrNHCE	TNTEEYIKRV		
msa521982.2{69_JM9130013}	VPRYLKRVEA	EENWLrNHCE	TNTEEYIKRV		
msa521982.2{69_090}	VPRYLKRVEA	EENWLkNHCE	TN-----		
msa521982.2{69_CJB110}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
msa521982.2{69_18RS21}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
msa521982.2{69_2603}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
msa521982.2{69_COH1}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
msa521982.2{69_M781}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
msa521982.2{69_1169NT}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
msa521982.2{69_M732}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
Consensus	*****	*****	*****		

Table 85: Comparative Sequences relating to SAG1361

SEQ ID NO. 8501

STRAIN 2603

atgagtaaacgacaaaatttaggaattagtaaaaaaggagcaattatatcagggctctca
 gtggcactaattgtagtaaataggtgggtttttatgggtacaatctcaacctaatagagt
 gcagtaaaaactaactacaaagtttttatgttagagaaggaggtgttcgtcctcaact
 cttttgacaggaagagctaaaggctaatacaagaacagtatgtgtattttgatgctaataaa
 ggttaatcgagcaactgtcacagttaaagtggtgataaaatcacagctggtcagcagtta
 gttcaabatgatacaacaactgcacaagcagcctacgacactgctaatacgtcaattaaat
 aaagttagcgcgtcagatttaataatctaagacaaacaggaagctctccagctatggaatca
 agtgatcaatctcttcatcatcacaaaggacaagggactcaatcgactagtggtgagcag
 aatcgctctacagcaaaattatcaaagtcagctaatgcttcatacaaccaacaactcaa
 gatttgaaatgatgcttatgcagatgcacagcgagaaagtaataaagcacaacaaagcattg
 aatgatactgttattacaagtgacgtatcagggacagttgttgaagttaatagtgatatt
 gatccagcttcaaaaactagtgcaagtactgtccatgtgacaaactgaaggtaaaactcaa
 gtacaaggaacgatgagtgagtgatgtttggctaatgttaaaaaagaccaggctgttaaa
 ataaaatctaaggtctatcctgacaaggaatgggaaggtaaaaatttcatatctcaaat
 tatccagaagcagaagcaacaacaatgactctaataacgggtctagtgtgttaaatat
 aaatataaagtagattacttagccctctcgatgcattaaaacaaggttttaccgctatca
 gttgaagtagtttaagggagataagcaccttatgtccctacaagttctgtgataaaca
 gataataaacactttgtttgggtatacaaatgattctaatacgtaaaatttccaaagttgaa
 gtcaaaattggtaagctgtagtgaagacacaagaattttatcaggtttgaaagcagga
 caaatcggtggttactaatccaagtaaaccttcaaggatgggcaaaaattgataatatt
 gaatcaatcgatcttaactctaataagaatcagaggtgaaa

SEQ ID NO. 8502

STRAIN 090

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAACTA
 CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
 AAGGTAATCGAGCAACTGTACAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAGCCTACG
 ACAGTCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
 AAGACAACAGGAAGTCTTCCAGCTATGGAATTAAGTGATCAATCTTCTTC
 ATCATACAAGGACAAGGACTCAATCGACTAGTGGTGGCAGCAATCGTC
 TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAAACTT
 CAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAAGTAATAAAGC
 ACAAAAAGCATTTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAAGTCAAGTA
 CTTGCTCATGTAGCAACTGAAGGTAACTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTTGGCTAATGTTAAAAAAGACCAAGCTGTTAAAAATAAAT
 CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAATTTTATATATCTCA
 AATTATCCAGAAGCAGAAGCAAAACAATGACTCTAATAACGGCTCTAG
 TGCTGTAATTTATAAATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAAACAAGGTTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTTATGTCTCCTACAAGTTCTGTGATAAAACAAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAGCA
 GGACAATCGTGGTTACTAATCCAAGTAAACCTTCAAGGATGGGCAAAA
 AATTGATAATATTGAATCAATCGATCTTAATCTAATAAGAAATCAGAGG

SEQ ID NO. 8503

STRAIN A909

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAA
 CTACAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTT
 TGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCT
 AATAAAGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCAC
 AGCTGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAGCCT
 ACGACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAAT
 CTAAAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTC
 ATCATCATACAAGGACAAGGGCTCAATCGACTAGTGGTGGCAGCAATC
 GTCTACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAA
 CTTCAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAAGTAATAA
 AGCACAAAAGCATTTGAATGATACTGTTATTACAAGTGACGTATCAGGGA
 CAGTTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAAGTCAAGTCA
 GTACTTGTCCATGTAGCAACTGAGGGTAACTCCAAGTACAAGGAACGAT
 GAGTGATATGATTTGGCTAATGTTAAAAAAGACCAAGTCTGTTAAAAATA
 AATCTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAATTTTATATATCT
 TCAAAATTATCCAGAAGCAGAAGCAAAACAATGACTCTAATAACGGCTC
 TAGTGCTGTAATTTATAAATAAAGTAGATATTACTAGCCCTCTCGATG
 CATTAACAAAGGTTTTACTGTATCAGTTGAAGTAGTTAATGGAGATAAG
 CACCTTATGTTCTTACAAGTTCTGTGACAAAACAAAGATAATAAACACTT
 TGTTTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCA
 AAATTTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAG
 GCAGGACAATCGTGGTTACTAATCCAAGCAAACTTCAAGGATGGGCA
 AAAAATTGATAATATTGAATCAATAGATCTAAGTCTAATAAGAAATCAG
 AGGTGAAA

SEQ ID NO. 8504

STRAIN H36B

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAATTA
 CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
 AAGGTAATCGAGCAACTGTACAGTTAAAGTGGGTGATAAAATCACAGC

Table 85: Comparative Sequences relating to SAG1361

TGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAGCCTACG
 ACACCTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
 AAGACAAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTCATC
 ATCATCACAAGGACAAGGGAAGTCAATCGACTAGTGGTGCAGCAATCGTC
 TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAAACCAACTT
 CAAGATTGTAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
 ACAAAAAGCATTGAATGATCTGTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGATATGATCCAGCTTCAAAAAGTCAAGTA
 CTGTGTCATGTAGCAACTGAAGGTAACTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTTGGCTAATGTAAAAAAGACAGGCTGTTAAATAAAAT
 CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAATTTTCATATATCTCA
 AATTATCCAGAAGCAGAAGCAAAACCAATGACTCTAATAACGGCTCTAG
 TGCTGTAAATTTATAAATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAAACAAGTTTACTGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTTATGTTCTACAAGTTCTGTGACAAACAAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
 GGACAAATCGTAGTTACTAATCCAAGTAAAGCTTCAAGGATGGGCAAAA
 AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
 TG

SEQ ID NO. 8505

STRAIN 18RS21

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAATA
 CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
 AAAGGTAATCGAGCAACTGTACAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAGCCTACG
 ACACCTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
 AAGACAAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTCTTC
 ATCATCACAAGGACAAGGGAAGTCAATCGACTAGTGGTGCAGCAATCGTC
 TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAAACCAACTT
 CAAGATTGTAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
 ACAAAAAGCATTGAATGATGATGTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGATATGATCCAGCTTCAAAAAGTCAAGTA
 CTGTGTCATGTAGCAACTGAAGGTAACTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTTGGCTAATGTTAAAAAAGACAGGCTGTTAAATAAAAT
 CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAATTTTCATATATCTCA
 AATTATCCAGAAGCAGAAGCAAAACAATGACTCTAATAACGGCTCTAG
 TGCTGTAAATTTATAAATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAAACAAGTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTTATGTCTCCTACAAGTTCTGTGATAAACAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
 GGACAAATCGTGGTTACTAATCCAAGTAAACCTTCAAGGATGGGCAAAA
 AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAG

SEQ ID NO. 8506

STRAIN M732

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAATTA
 CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
 AAAGGTAATCGAGCAACTGTACAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAGCCTACG
 ACACCTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
 AAGACAAACAGGGAGTTTCCAGCTATGGAATCAAGTGATCAATCTTCATC
 ATCATCACAAGGACAAGGGAAGTCAATCGACTAGTGGTGCAGCAATCGTC
 TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAAACCAACTT
 CAAGATTGTAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
 ACAAAAAGCATTGAATGATGATGTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGATATGATCCAGCTTCAAAAAGTCAAGTA
 CTGTGTCATGTAGCAACTGAAGGTAACTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTTGGCTAATGTTAAAAAAGATCAGGCTGTTAAATAAAAT
 CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAATTTTCATATATCTCA
 AATTATCCAGAAGCAGAAGCAAAACAATGACTCTAATAACGGCTCTAG
 TGCTGTAAATTTATAAATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAAACAAGTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTTATGTCTCCTACAAGTTCTGTGATAAACAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
 GGACAAATCGTGGTTACTAATCCAAGTAAACCTTCAAGGATGGGCAAAA
 AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
 TGAA

SEQ ID NO. 8507

STRAIN COH1

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAAAC
 TAATTACAAGTTTAAATGTTAGAGAAGGAAGTGTTCGTCTCAACTC
 TTTTGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTGAT
 GCTAATAAAGGTAATCGAGCAACTGTACAGTTAAAGTGGGTGATAAAAT
 CACAGCTGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAG
 CTTACGACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAAT
 AATCTAAAGACAAACAGGAGTTTTCAGCTATGGAATCAAGTGATCAATC

Table 85: Comparative Sequences relating to SAG1361

TTCATCATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGA
 ATCGTCTACAGCAAAATTTATCAAAGTCAAGCTAATGCTTCATACAACCAA
 CAACCTTCAAGATTGAATGATGCTTATGCAGATGCACAGGCAGAAAGTAAA
 TAAAGCACAAAAGCATTTGAATGATAGTCTTATTAACAAGTGACGTATCAG
 GGACAGTTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAAGTAGT
 CAAGTACTTGTCCATGTAGCAACTGAAGGTAAACTCCAAGTACAAGGAAC
 GATGAGTGAGTATGATTGGCTAATGTTAAAAAAGATCAGGCTGTTAAAA
 TAAAAATCTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAAATTTATAT
 ATCTCAAATTTATCCAGAAGCAGAAGCAAACAACATGACTCTAATAACGG
 CTCTAGTGTCTGTAATTTATAATATAAAGTAGATATTACTAGCCCTCTCG
 ATGCATTAAAAACAGGTTTACCGTATCAGTTGAAGTAGTTAATGGAGAT
 AAGCACCTTATTGTCCCTACAAGTTCTGTGATAAAACAAAGATAATAAACA
 CTTTGTGTTGGGTATACAATGATTTCTAATCGTAAATTTCCAAGTTGAAG
 TCAAAATTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTG
 AAAGCAGGACAAATCGTGGTTACTAATCCAGCAAAATTTCAAGGATGG
 GCAAAAAATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAAT
 CAGAGGTGAA

SEQ ID NO. 8507

STRAIN M781

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGAGTAAAACTAATTA
 CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCTTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTTGATTTTGATGCTAAT
 AAAGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAGCCTACG
 ACACGTCTAATCGTCAATTAATAAAGTAGCGCGTCAGATTAAATAATCTA
 AAGACAACAGGGAGTTTCCAGCTATGGAATCAAGTGATCAATCTTCATC
 ATCATCACAGGACAAGGGACTCAATCGACTAGTGGTGCAGCAATCGTC
 TACAGCAAAATTTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACCT
 CAAGATTTGAATGATGCTTATGTCAGATGCACAGGCAGAAAGTAAATAAAGC
 ACAAAAAGCATTGAATGATGCTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAAGTAGTCAAGTA
 CTTGTCATGATAGCAACTGAAGGTAACTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTTGGCTAATGTTAAAAAAGATCAGGCTGTTAAATAAAT
 CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAATTTTATATATCTCA
 AATTATCCAGAAGCAGAAGCAACAACAATGACTCTAATAACGGCTCTAG
 TGCTGTAAATTTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAAACAAGTTTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTTATTGTCCCTACAAGTTCTGTGATAAACAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
 GGACAAATCGTGGTTACTAATCCAAGCAAACTTTCAAGGATGGGCAAAA
 AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
 TGAA

SEQ ID NO. 8508

STRAIN CJB110

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGAGTAAAACTAATTA
 CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCTTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTTGATTTTGATGCTAAT
 AAAGGTAATCGAGCAACTGTCACAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAGCCTACG
 ACACGTCTAATCGTCAATTAATAAAGTAGCGCGTCAGATTAAATAATCTA
 AAGACAACAGGAAGTCTTCCAGCTATGGAATTAAGTGATCAATCTTCTTC
 ATCATCACAGGACAAGGGACTCAATCGACTAGTGGTGCAGCAATCGTC
 TACAGCAAAATTTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACCT
 CAAGATTTGAATGATGCTTATGTCAGATGCACAGGCAGAAAGTAAATAAAGC
 ACAAAAAGCATTGAATGATGCTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAAGTAGTCAAGTA
 CTTGTCATGATAGCAACTGAAGGTAACTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTTGGCTAATGTTAAAAAAGACCAGGCTGTTAAATAAAT
 CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAATTTTATATATCTCA
 AATTATCCAGAAGCAGAAGCAACAACAATGACTCTAATAACGGCTCTAG
 TGCTGTAAATTTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAAACAAGTTTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTTATTGTCCCTACAAGTTCTGTGATAAACAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
 GGACAAATCGTGGTTACTAATCCAAGTAAACCTTTCAAGGATGGGCAAAA
 AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
 TGA

SEQ ID NO. 8509

STRAIN I169NT

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGAGTAAAACT
 AACTACAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCT
 TTTGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTTGATTTTGATG
 CTAATAAAGGTAATCGAGCAACTGTCACAGTTAAAGTGGGTGATAAAATC
 ACAGCTGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAGC
 CTACGACACTGCTAATCGTCAATTAATAAAGTAGCGCGTCAGATTAAATA
 ATCTAAAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCT
 TCTTCATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCAGCAAA
 TCGTCTACAGCAAAATTTATCAAAGTCAAGCTAATGCTTCATACAACCAAC

Table 85: Comparative Sequences relating to SAG1361

AACTTCAAGATTGTAATGATGCTTATGCAGATGCACAGGCAGAAGTAAT
AAAGCACAAAAGTGAATGAATGATATGTTATTACAAGTGACGTATCAGG
CAGAGTTTGAAGTTAATAGTGATATTGTCAGCTTCAAAAACTAGTC
AAGTACTTGTCCATGTAGCACTGAAGGTAACCTCCAAGTACAAGGAACG
ATGAGTGAGTATGATTTGGCTAATGTTAAAAAAGCAGCGCTGTTTAAAT
AAAACTAAGGTCATCTCTGACAAAGGAATGGGAAGGTAATAATTCATTA
TCTCAAATTTATCCAGAAGCAGAAGCAACAACAATGACTCTAATAACGGC
TCTAGTGCTGTAAATATAAATATAAGATAGATATTACTAGCCCTCTCGA
TGCTATAAAAACAGGTTTATCCGTTATCAGTTGAAGTAGTTATGGAGATA
AGCACTTATTTGCCCTACAAGTTCTGTGATAAACAAAGATAATTAACAC
TTTGTTTGGGTATAACAATGATTTCTAATCGTAAATTTCCAAAGTTGAAGT
CAAAATTTGTAAGCTGATGCTAAGACAGAGAAATTTTATCAGGTTTGA
AAGCAGGACAATTCGTGGTTACTAATCAAAGTAAACCTTCAAGGATGGG
CAAAAATTGATAATTTGAATCAATCGATCTTAACCTTAATAAGAAATC
AGAGGTGAA

SEQ ID NO. 8510

STRAIN JM9130013

TTTTTATGGGTACAATCTCAACCTTAATAAGAGTGCAGTAAAACTAACTCA
CAAAGTTTTAATGCTTAGAGCAAGGAAGTGTTCGTCTCAACTCTTTTGA
CAGGAAAAGCTTAGGCTAATCAAGAAGCAGTATGCTGTTATTGTAGTCGAA
AAAGTGAATTCGAGCAACTGCTTAGCATGTAAAGTGGGTGATAAAAATCACAGC
TGGTCAGCACTTAGTTCAATATGATACAACACTGCACAGCAGCCTACG
ACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAAATAATCTA
AAGACAACAGGAAGTCTTCAGCATTTGAATCAAGTGATCAATCTTCATCT
ATCATCAACAGGACAGGGGGCTCAATCGACTAGTGTGGCAGCAATCGTC
TACAGCAAAATTAACAACTCAAGCTAGTATGCTTCTACAACCAACAACTT
CAAGAAATTGAATGATGCTTATGCAAGTGCACAGGCAGAGTAATAAAGC
ACAAAAGCATTGAATGATATCTGTTATTACAAGTACGCTATCAGGACAG
TTGTTGAAGTAAATAGTGATTAATGATCAGCTCAAAAACATGTCGAAGTA
CTTGTCTAGTGTACCAACTGAGGGTTAAACTCCAAGTACAAGGAACGATGAG
TGAGTATGATTTGGCTAATGTTAAAAAAGACCAGTCTGTTAAAAATAAAAT
CTAAGGTCTATGCTGACAAGGAATGGGAAGTGTAATTTCATATATCTCA
AATTATCAGAAGCAGCAAGACAACCAATAGCTCAATTAACCGCTCTAG
TGCTGTAAATTAATAAATATAAAGTAGATATTATGACCCCTCTCATAGTAT
TAAAAACAAGGTTTACTGTATCAGTTGAAGTAGTTAATGGAGATGACAC
CTTATTGTTCTCAACAGTTCTGTGACAAACAAGATAATAAACACTTTGT
TTGGGTATCAATGATCTAATCGTAAAAATTTCCAAGTGTGAAGTCAAAA
TTGGTAAAGCTGATGCTAAGACAAGAAATTTTATCAGGTTTGAAGACA
GGACAATCGTGGTTACTAATCCAAGCAAAACTTTCAAGGATGGGCAAAA
AATTGATAATATTGAATCAATAGATCTTAAGTCTAATAAGAAATCAGAG
TGAAA

PRETTY of: /biotmp/msa363690.2{*} March 31, 2003 07:01 ..

	1					50
msa363690.2{690_COH1}	~	~	~	~	~	~
msa363690.2{690_M732}	~	~	~	~	~	~
msa363690.2{690_M781}	~	~	~	~	~	~
msa363690.2{690_090}	~	~	~	~	~	~
msa363690.2{690_CJB110}	~	~	~	~	~	~
msa363690.2{690_1169NT}	~	~	~	~	~	~
msa363690.2{690_18R921}	~	~	~	~	~	~
msa363690.2{690_2603}	atgagtaaac	gacaaaattt	aggaattagt	aaaaaaggag	caattatatt	
msa363690.2{690_A909}	~	~	~	~	~	~
msa363690.2{690_JM9130013}	~	~	~	~	~	~
msa363690.2{690_H36B}	~	~	~	~	~	~
Consensus	*****	*****	*****	*****	*****	*****

	51				100
msa363690.2{690_COH1}	~~~~~	~~~~~	~~~~~	~~~~~TTT	TTATGGGTAC
msa363690.2{690_M732}	~~~~~	~~~~~	~~~~~	~~~~~TTT	TTATGGGTAC
msa363690.2{690_M781}	~~~~~	~~~~~	~~~~~	~~~~~TTT	TTATGGGTAC
msa363690.2{690_090}	~~~~~	~~~~~	~~~~~	~~~~~TTT	TTATGGGTAC
msa363690.2{690_CJB110}	~~~~~	~~~~~	~~~~~	~~~~~TTT	TTATGGGTAC
msa363690.2{690_1169NT}	~~~~~	~~~~~	~~~~~	~~~~~TTT	TTATGGGTAC
msa363690.2{690_18RS21}	~~~~~	~~~~~	~~~~~	~~~~~TTT	TTATGGGTAC
msa363690.2{690_2603}	agggcctc	gtggcact	ttgtagta	aggtggcTTT	TTATGGGTAC
msa363690.2{690_A909}	~~~~~	~~~~~	~~~~~	~~~~~TTT	TTATGGGTAC
msa363690.2{690_JM9130013}	~~~~~	~~~~~	~~~~~	~~~~~TTT	TTATGGGTAC
msa363690.2{690_H36B}	~~~~~	~~~~~	~~~~~	~~~~~TTT	TTATGGGTAC
Consensus	*****	*****	*****	*****	*****

	101	150
msa363690.2{690_COH1}	AATCTCAACC	TAATAAGAGT GCAGTAAAAA CTAAtTACAA AGTTTTTAAT
msa363690.2{690_M732}	AATCTCAACC	TAATAAGAGT GCAGTAAAAA CTAAtTACAA AGTTTTTAAT
msa363690.2{690_M781}	AATCTCAACC	TAATAAGAGT GCAGTAAAAA CTAAtTACAA AGTTTTTAAT
msa363690.2{690_O90}	AATCTCAACC	TAATAAGAGT GCAGTAAAAA CTAAtTACAA AGTTTTTAAT
msa363690.2{690_CJB110}	AATCTCAACC	TAATAAGAGT GCAGTAAAAA CTAAtTACAA AGTTTTTAAT
msa363690.2{690_1169NT}	AATCTCAACC	TAATAAGAGT GCAGTAAAAA CTAAtTACAA AGTTTTTAAT
msa363690.2{690_18RS21}	AATCTCAACC	TAATAAGAGT GCAGTAAAAA CTAAtTACAA AGTTTTTAAT
msa363690.2{690_2603}	AATCTCAACC	TAATAAGAGT GCAGTAAAAA CTAAtTACAA AGTTTTTAAT

Table 85: Comparative Sequences relating to SAG1361

msa363690.2{690_A909}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAcTACAA	AGTTTTTAAAT
msa363690.2{690_JM9130013}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAcTACAA	AGTTTTTAAAT
msa363690.2{690_H36B}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAcTACAA	AGTTTTTAAAT
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	151	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	200
msa363690.2{690_M732}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_M781}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_090}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_CJB110}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_1169NT}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_18RS21}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_2603}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_A909}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_JM9130013}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_H36B}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	201	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	250
msa363690.2{690_M732}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_M781}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_090}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_CJB110}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_1169NT}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_18RS21}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_2603}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_A909}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_JM9130013}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_H36B}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	251	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	300
msa363690.2{690_M732}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_M781}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_090}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_CJB110}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_1169NT}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_18RS21}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_2603}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_A909}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_JM9130013}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_H36B}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	301	GTTCAATATG	ATACAACAAC	TGCACAAGCA	350
msa363690.2{690_M732}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_M781}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_090}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_CJB110}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_1169NT}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_18RS21}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_2603}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_A909}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_JM9130013}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_H36B}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	351	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	400
msa363690.2{690_M732}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_M781}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_090}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_CJB110}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_1169NT}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_18RS21}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_2603}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_A909}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_JM9130013}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_H36B}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	401	GTtTTCCAGC	TATGGAATcA	AGTGATCAAT	450
msa363690.2{690_M732}	GTtTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcATCATC	ATCACAAGGA
msa363690.2{690_M781}	GTtTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcATCATC	ATCACAAGGA
msa363690.2{690_090}	GTtTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcATCATC	ATCACAAGGA
msa363690.2{690_CJB110}	GTtTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcATCATC	ATCACAAGGA
msa363690.2{690_1169NT}	GTtTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcATCATC	ATCACAAGGA
msa363690.2{690_18RS21}	GTtTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcATCATC	ATCACAAGGA

Table 85: Comparative Sequences relating to SAG1361

msa363690.2{690_2603}	GTcTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTCtTCATC	ATCACAAGGA
msa363690.2{690_A909}	GTcTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTCaTCATC	ATCACAAGGA
msa363690.2{690_JM9130013}	GTcTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTCaTCATC	ATCACAAGGA
msa363690.2{690_H36B}	GTcTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTCaTCATC	ATCACAAGGA
Consensus	***-*****	*****-*	*****	*****-*****	*****
msa363690.2{690_COH1}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_M732}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_M781}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_090}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_CJB110}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_1169NT}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_18RS21}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_2603}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_A909}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_JM9130013}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_H36B}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
Consensus	*****-***	*****	*****	*****	*****
msa363690.2{690_COH1}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_M732}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_M781}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_090}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_CJB110}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_1169NT}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_18RS21}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_2603}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_A909}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_JM9130013}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_H36B}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_M732}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_M781}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_090}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_CJB110}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_1169NT}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_18RS21}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_2603}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_A909}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_JM9130013}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_H36B}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_M732}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_M781}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_090}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_CJB110}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_1169NT}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_18RS21}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_2603}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_A909}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_JM9130013}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_H36B}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_M732}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_M781}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_090}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_CJB110}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_1169NT}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_18RS21}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_2603}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_A909}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_JM9130013}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_H36B}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_M732}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_M781}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_090}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_CJB110}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_1169NT}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG

Table 85: Comparative Sequences relating to SAG1361

msa363690.2{690_18RS21}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTGG
msa363690.2{690_2603}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTGG
msa363690.2{690_A909}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTGG
msa363690.2{690_JM9130013}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTGG
msa363690.2{690_H36B}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTGG
Consensus	*****-*	*****	*****	*****	*****
msa363690.2{690_COH1}	751	AAAAAGATCA	GgCTGTTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_M732}	GCTAATGTtA	AAAAAGATCA	GgCTGTTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_M781}	GCTAATGTtA	AAAAAGATCA	GgCTGTTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_090}	GCTAATGTtA	AAAAAGATCA	GgCTGTTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_CJB110}	GCTAATGTtA	AAAAAGATCA	GgCTGTTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_1169NT}	GCTAATGTtA	AAAAAGATCA	GgCTGTTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_18RS21}	GCTAATGTtA	AAAAAGATCA	GgCTGTTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_2603}	GCTAATGTtA	AAAAAGATCA	GgCTGTTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_A909}	GCTAATGTtA	AAAAAGATCA	GgCTGTTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_JM9130013}	GCTAATGTtA	AAAAAGATCA	GgCTGTTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_H36B}	GCTAATGTtA	AAAAAGATCA	GgCTGTTAA	ATAAAATCTA	AGGTCTATCC
Consensus	*****-*	*****	*-*****	*****	*****
msa363690.2{690_COH1}	801	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT
msa363690.2{690_M732}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_M781}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_090}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_CJB110}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_1169NT}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_18RS21}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_2603}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_A909}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_JM9130013}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_H36B}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	851	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC
msa363690.2{690_M732}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_M781}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_090}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_CJB110}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_1169NT}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_18RS21}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_2603}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_A909}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_JM9130013}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_H36B}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	901	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA
msa363690.2{690_M732}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_M781}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_090}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_CJB110}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_1169NT}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_18RS21}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_2603}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_A909}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_JM9130013}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_H36B}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	951	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT
msa363690.2{690_M732}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_M781}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_090}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_CJB110}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_1169NT}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_18RS21}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_2603}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_A909}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_JM9130013}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_H36B}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
Consensus	***-*****	*****	*****	*****	*****
msa363690.2{690_COH1}	1001	CAAGTTCTGT	GatAAACAAA	GATAATAAAC	ACTTTGTTTG
msa363690.2{690_M732}	CAAGTTCTGT	GatAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAAT
msa363690.2{690_M781}	CAAGTTCTGT	GatAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAAT
msa363690.2{690_090}	CAAGTTCTGT	GatAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAAT
msa363690.2{690_CJB110}	CAAGTTCTGT	GatAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAAT

Table 85: Comparative Sequences relating to SAG1361

msa363690.2{690_1169NT}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_18RS21}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_2603}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_A909}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_JM9130013}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_H36B}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_M732}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_M781}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_090}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_CJB110}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_1169NT}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_18RS21}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_2603}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_A909}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_JM9130013}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_H36B}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_M732}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_M781}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_090}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_CJB110}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_1169NT}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_18RS21}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_2603}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_A909}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_JM9130013}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_H36B}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_M732}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_M781}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_090}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_CJB110}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_1169NT}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_18RS21}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_2603}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_A909}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_JM9130013}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_H36B}	TTACTAATCC	AAGtAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
Consensus	*****	***-***-*	*****	*****	*****
msa363690.2{690_COH1}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_M732}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_M781}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_090}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_CJB110}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_1169NT}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_18RS21}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_2603}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	aA
msa363690.2{690_A909}	GAATCAATaG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	aA
msa363690.2{690_JM9130013}	GAATCAATaG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	aA
msa363690.2{690_H36B}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtg-	~
Consensus	*****	*****	*****	*****	*****

SEQ ID NO. 8511

STRAIN 2603 frame: 1

MSKRQNLGI SKKGAI ISGLSVALIVVIGGFLVWQSQPNKSAVKTNKYVFNVRREGSVSSST
 LLTGKAKANQEYVYFDANKGNRATVTVKVGDKITAGQQLVQYDTTAAQAAAYDTANRQLN
 KVARQINNLKTTGSLPAMESSDQSSSSSQGGTQSTSGATNRLQONYQSQANASYNQQLQ
 DLNDAYADAQAEVNKAQKALNDTVITSDVSGTVVEVNSDIDPASKTSQVLVHVATEGKLQ
 VQGTMSYDLANVKKDQAVIKSKVYPDKWEKGKISYISNYPEAEANNNDNNSSSAVNY
 KYKVDITSPLDALKQGFVTSVEVNGDKHLIVPTSSVINKDNKHFVWVYNDNSNRKISKVE
 VKIGKADAKTQEILSGLKAGQIVVTNPSKTFKDGQKIDNIESIDLNSNKKSEVK

SEQ ID NO. 8512

STRAIN 090 frame: 1

FLWVQSQPNKSAVKTNKYVFNVRREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTAAQAAAYDTANRQLNKLKTTGSLPAMESSDQSSSSSQ
 GGTTQSTSGATNRLQONYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSYDLANVKKDQAVIKSKVYPDK
 EWEGKISYISNYPEAEANNNDNNSSSAVNYKYKVDITSPLDALKQGFVTSVEVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLNSNKKSE

Table 85: Comparative Sequences relating to SAG1361

SEQ ID NO. 8513

STRAIN A909 frame: 1

FLWVQSQPNKSAVKTNKYKFNVRREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGAQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKQDQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVTNKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8514

STRAIN H36B frame: 1

FLWVQSQPNKSAVKTNKYKFNVRREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKQDQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVTNKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 AFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8515

STRAIN I8RS21 frame: 1

FLWVQSQPNKSAVKTNKYKFNVRREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKQDQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSE

SEQ ID NO. 8516

STRAIN M732 frame: 1

FLWVQSQPNKSAVKTNKYKFNVRREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKQDQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8517

STRAIN COH1 frame: 1

FLWVQSQPNKSAVKTNKYKFNVRREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKQDQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8518

STRAIN M781 frame: 1

FLWVQSQPNKSAVKTNKYKFNVRREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKQDQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8519

STRAIN M781 frame: 1

FLWVQSQPNKSAVKTNKYKFNVRREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKQDQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8520

STRAIN CJB110 frame: 1

FLWVQSQPNKSAVKTNKYKFNVRREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKQDQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8521

Table 85: Comparative Sequences relating to SAG1361

STRAIN 1169NT frame: 1

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FLWVQSQPNKSAVKTNKYVFNREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
GQGTQSTSGATNRLQONQYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSYDLANVKKDQAVKI KSKVYPPDK
EWEGKISYISNYPEAEANNDNSNGSSAVNYKYKVDITSPLDALKQGTFSVEVNVGDKH
LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
TFKDGQKIDNIESIDLNSNKKSEV

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SEQ ID NO. 8522

STRAIN JM9130013 frame: 1

```

FLWVQSQPNKSAVKTNKYVFNREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
GQGAQSTSGATNRLQONQYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSYDLANVKKDQAVKI KSKVYPPDK
EWEGKISYISNYPEAEANNDNSNGSSAVNYKYKVDITSPLDALKQGTFSVEVNVGDKH
LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
TFKDGQKIDNIESIDLNSNKKSEV

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PRETTY of: /biotmp/msa375805.2{*} April 1, 2003 02:58 ..

msa375805.2{690_COH1}	1	50
msa375805.2{690_M732}	-----F	LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_M781}	-----F	LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_090}	-----F	LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_CJB110}	-----F	LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_1169NT}	-----F	LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_18RS21}	-----F	LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_2603}	mskrqnlgis kkgaiisgls valivviggf	LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_A909}	-----F	LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_JM9130013}	-----F	LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_H36B}	-----F	LWVQSQPNKS AVKTNKYVFN
Consensus	*****	*****
msa375805.2{690_COH1}	51	100
msa375805.2{690_M732}	VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV	GDKITAGQQL
msa375805.2{690_M781}	VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV	GDKITAGQQL
msa375805.2{690_090}	VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV	GDKITAGQQL
msa375805.2{690_CJB110}	VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV	GDKITAGQQL
msa375805.2{690_1169NT}	VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV	GDKITAGQQL
msa375805.2{690_18RS21}	VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV	GDKITAGQQL
msa375805.2{690_2603}	VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV	GDKITAGQQL
msa375805.2{690_A909}	VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV	GDKITAGQQL
msa375805.2{690_JM9130013}	VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV	GDKITAGQQL
msa375805.2{690_H36B}	VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV	GDKITAGQQL
Consensus	*****	*****
msa375805.2{690_COH1}	101	150
msa375805.2{690_M732}	VQYDITTTAQ AYDTANRQLN KVARQINNLT TTGSFPAMES	SDQSSSSSQ
msa375805.2{690_M781}	VQYDITTTAQ AYDTANRQLN KVARQINNLT TTGSFPAMES	SDQSSSSSQ
msa375805.2{690_090}	VQYDITTTAQ AYDTANRQLN KVARQINNLT TTGSFPAMES	SDQSSSSSQ
msa375805.2{690_CJB110}	VQYDITTTAQ AYDTANRQLN KVARQINNLT TTGSFPAMES	SDQSSSSSQ
msa375805.2{690_1169NT}	VQYDITTTAQ AYDTANRQLN KVARQINNLT TTGSFPAMES	SDQSSSSSQ
msa375805.2{690_18RS21}	VQYDITTTAQ AYDTANRQLN KVARQINNLT TTGSFPAMES	SDQSSSSSQ
msa375805.2{690_2603}	VQYDITTTAQ AYDTANRQLN KVARQINNLT TTGSFPAMES	SDQSSSSSQ
msa375805.2{690_A909}	VQYDITTTAQ AYDTANRQLN KVARQINNLT TTGSFPAMES	SDQSSSSSQ
msa375805.2{690_JM9130013}	VQYDITTTAQ AYDTANRQLN KVARQINNLT TTGSFPAMES	SDQSSSSSQ
msa375805.2{690_H36B}	VQYDITTTAQ AYDTANRQLN KVARQINNLT TTGSFPAMES	SDQSSSSSQ
Consensus	*****	*****
msa375805.2{690_COH1}	151	200
msa375805.2{690_M732}	QGTQSTSGAT NRLQONQYQSQ ANASYNQQLQ DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_M781}	QGTQSTSGAT NRLQONQYQSQ ANASYNQQLQ DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_090}	QGTQSTSGAT NRLQONQYQSQ ANASYNQQLQ DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_CJB110}	QGTQSTSGAT NRLQONQYQSQ ANASYNQQLQ DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_1169NT}	QGTQSTSGAT NRLQONQYQSQ ANASYNQQLQ DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_18RS21}	QGTQSTSGAT NRLQONQYQSQ ANASYNQQLQ DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_2603}	QGTQSTSGAT NRLQONQYQSQ ANASYNQQLQ DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_A909}	QGTQSTSGAT NRLQONQYQSQ ANASYNQQLQ DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_JM9130013}	QGTQSTSGAT NRLQONQYQSQ ANASYNQQLQ DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_H36B}	QGTQSTSGAT NRLQONQYQSQ ANASYNQQLQ DLNDAYADAQ	AEVNKAQKAL
Consensus	***-*****	*****
msa375805.2{690_COH1}	201	250
msa375805.2{690_M732}	NDTVITSDVS GTVVEVNSDI DPASKTSQVL VHVATEGKLQ	VQGTMSYIDL
msa375805.2{690_M781}	NDTVITSDVS GTVVEVNSDI DPASKTSQVL VHVATEGKLQ	VQGTMSYIDL
msa375805.2{690_090}	NDTVITSDVS GTVVEVNSDI DPASKTSQVL VHVATEGKLQ	VQGTMSYIDL

Table 85: Comparative Sequences relating to SAG1361

msa375805.2{690_CJB110}	NDTVITSQVLS	GTVEVNSDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSSEYDL
msa375805.2{690_1169NT}	NDTVITSQVLS	GTVEVNSDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSSEYDL
msa375805.2{690_18RS21}	NDTVITSQVLS	GTVEVNSDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSSEYDL
msa375805.2{690_2603}	NDTVITSQVLS	GTVEVNSDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSSEYDL
msa375805.2{690_A909}	NDTVITSQVLS	GTVEVNSDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSSEYDL
msa375805.2{690_JM9130013}	NDTVITSQVLS	GTVEVNSDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSSEYDL
msa375805.2{690_H36B}	NDTVITSQVLS	GTVEVNSDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSSEYDL
Consensus	*****	*****	*****	*****	*****
	251				300
msa375805.2{690_COH1}	ANVKKDQaVK	IKSKVYPDK	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_M732}	ANVKKDQaVK	IKSKVYPDK	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_M781}	ANVKKDQaVK	IKSKVYPDK	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_090}	ANVKKDQaVK	IKSKVYPDK	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_CJB110}	ANVKKDQaVK	IKSKVYPDK	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_1169NT}	ANVKKDQaVK	IKSKVYPDK	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_18RS21}	ANVKKDQaVK	IKSKVYPDK	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_2603}	ANVKKDQaVK	IKSKVYPDK	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_A909}	ANVKKDQaVK	IKSKVYPDK	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_JM9130013}	ANVKKDQaVK	IKSKVYPDK	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_H36B}	ANVKKDQaVK	IKSKVYPDK	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
Consensus	*****	*****	*****	*****	*****
	301				350
msa375805.2{690_COH1}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_M732}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_M781}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_090}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_CJB110}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_1169NT}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_18RS21}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_2603}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_A909}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_JM9130013}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_H36B}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
Consensus	*****	*****	*****	*****	*****
	351				400
msa375805.2{690_COH1}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_M732}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_M781}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_090}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_CJB110}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_1169NT}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_18RS21}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_2603}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_A909}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_JM9130013}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_H36B}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
Consensus	*****	*****	*****	*****	*****
	401				414
msa375805.2{690_COH1}	ESIDLKSNKK	SEv-			
msa375805.2{690_M732}	ESIDLKSNKK	SEv-			
msa375805.2{690_M781}	ESIDLKSNKK	SEv-			
msa375805.2{690_090}	ESIDLKSNKK	SEv-			
msa375805.2{690_CJB110}	ESIDLKSNKK	SEv-			
msa375805.2{690_1169NT}	ESIDLKSNKK	SEv-			
msa375805.2{690_18RS21}	ESIDLKSNKK	SEv-			
msa375805.2{690_2603}	ESIDLKSNKK	SEvK			
msa375805.2{690_A909}	ESIDLKSNKK	SEvK			
msa375805.2{690_JM9130013}	ESIDLKSNKK	SEvK			
msa375805.2{690_H36B}	ESIDLKSNKK	SEv-			
Consensus	*****	***			

Table 86: Comparative Sequences relating to SAG1393

SEQ ID NO. 8601

STRAIN 2603

atgaaaaaattggaattattgtcctcacactactgacctcttttttggtatcttgcgga
 caacaaactaaacaagaaagcactaaaacaactatttctaaaatgctaaaattgaaggc
 ttcacctattatggaaaaattcctgaaaatccgaaaaagtaatttttacatattct
 tacactgggtatttattaaaactaggtgttaattgttcaagttacagtttagacttagaa
 aaagatagcccggttttttggttaaacactgaagaagctaaaaaattaactgctgatgat
 acagaagctattgcccgcacaaaaacctgatttaatacatggttttcgatcaagatccaaac
 atcaatactctgaaaaaaattgacccaactttagttatataatattggtgcacaaaattat
 ttagatatgatgccagccttggggaaagtattcggtaaagaaaaagaagctaatacagtggtg
 gttagccaatggaaaaactaaaactctcgctgtcaaaaaagatttacaccatatcttaag
 cctaacactacttttactattatggatttttatgataaaaaatctattttatggttaatt
 aattttggacgcggtggagaactaatctatgattcactaggttatgctgccccagaaaaa
 gtcaaaaaagatgtcttttaaaaaagggtggtttaccgtttcgcaagaagcaatcggtgat
 tacgttggagattatgcccttgttaataataacaaaacgactaaaaagcagcttcatca
 cttaagaaagtgatgtctggaagaatttaccagctgtcaaaaaagggcacatcatagaa
 agtaactacgagctgttttatttctctgacctctatctttagaagctcaattaaaatca
 tttacaaaggctatcaagaaaaatacaaat

SEQ ID NO. 8602

STRAIN 090

GAAGGCTTCACCTATTATGGAAAAATTCCTGAAAAATCCGAAAAAGTAAT
 TAATTTTACATATTCTTACACTGGGTATTTATTAATACTAGGTGTTAATG
 TTTCAAGTTACAGTTTAGACTTAGAAAAAGATAGCCCCGTTTTTGGTAAAG
 CAACTGAAAGAGCTAAAAAATTAACCTGCTGATGATACAGAAGCTATTGTC
 CGCACAAAAACCTGATTTAATCATGGTTTTTCGATCAAGATCCAAACATCA
 ATACTCTGAAAAAAATGACCAACTTTAGTTATTAATATGGTGCACAA
 AATTATTTAGATATGATGCCAGCCTTGGGAAAGTATTCGGTAAAGAAAA
 AGAAGCTAATCAGTGGTTAGCCAATGGAAAACTAAAACTCTCGCTGCCA
 AAAAAAGATTTACCATATCTTAAAGCCTAACACTACTTTTACTATTATG
 GATTTTATGATAAAAAATATCTATTTATATGGTAATAATTTTGGACGCGG
 TGGAGAACTAATCTATGATTCACTAGGTATGCTGCCCAgAAAAAGTCA
 AAAAAAGATGTCTTTAAAAAAGGGTGGTTTACCCTTTTCgCAAGAAGCAATC
 GGTGATTACGTTGGAGATTATGCCCTTGTAAATATAACAAAACGACTAA
 AAAAGCAGCTTCatcACTTAAAGAAAGTGATGTCTGGAAGAATTTACCAG
 CTGTCAAAAAAGGGCACATCATAGAAAGTAacTACGACGTGTTTTATTTC
 TCTGACCTCTATCTTTTAGAAGCTCAATTAAAAATCATTTACAAA

SEQ ID NO. 8603

STRAIN A909

GAAGGCTTCACCTATTATGGAAAAATTCCTG
 AAAATCCGAAAAAGTAATTAATTTTACATATTCTTACACTGGATATTTA
 TTAAACTAGGAGTTAATGTTTCAAGTTACAGTTTAGACTTAGAAAAAGA
 TAgCCCCGTTTTTGGTAAaCAACTGAAAGGAGCTAAAAAATTAACCTGCTG
 ATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAaTCATGGTTTTT
 GATCAAGATCCAAACATCAATACTCTGAAAAAATGACCAACTTTTAGT
 TATTAAATATGGTGACAAAAATTTTATGATaTgATGCCAGCTTTGGGGA
 AAGTATTCGGTAAAGAAAAAGAGCTAATCAGTGGGTTAGCCaTGGAAA
 ACTAAAACTCTCGCTGCCAAAAAAGATTACACCATATCTTAAACCTAA
 CACTACTTTTACCATTATGGATTTTTATGATAAAAAATATCTATTTATATG
 GTAATAATTTTGGACGCGGTGAGAACTAATCTATGATTCACTAGGTTAT
 GCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAAAGGGTGGTTTAC
 CGTTTCGCAAGAAAGCAATCGGTgATTACGTTGGAGATTATGCCCTTGTTA
 ATATAACAAAACGACTAAAAAAGCAGCTTCATCACTTAAAGAAAGTGAT
 GTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACATCATAGAAAGTAA
 CTACGACGTGTTTTATTCTCTGACCCTcTATCTTTAGAAGCTCAATTAA
 AATCATTTACAAA

SEQ ID NO. 8604

STRAIN H36B

GAAGGCTTCACCTATTATGGAAAA
 ATTCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACACTGG
 ATATTTATTAAAACTAGGAGTTAATGTTTCAAGTTACAGTTTAGACTTAG
 AAAAAAGATAgCCCCGTTTTTGGTAAgCAACTGAAAGGAGCTAAAAAATTA
 ACTGCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAaTCAT
 GGTTTTTATGATCAAGATCCAAACATCAATACTCTGAAAAAATGACCAAA
 CTTTAGTTATTAAATATGGTGACAAAAATTTTATGATaTgATGCCAGCT
 TTGGGGAaAGTATTCGGTAAAGAAAAAGAGCTAATCAGTGGGTTAGCCA
 ATGGA AAACTAAAACTCTCGCTGCCAAAAAAGATTACACCATATCTTAA
 GGCCTaACaCTACTTTTACTATTATAGatTTTTATGATAAAAAATATCTAT
 TTTATATGTAATAATTTTGGACGCGGTGGAgAACTAATCTATGATcCACT
 AGGTTATGCTGCCCAgAAAAAGTCAAAAAAGATGTCTTTAAAAAAGGGT
 GGTTTACCCTTTTCgCAAGAAGCAATCGGTgATTACGTTGGAGATTATGCC
 CTTGTTAATATAAAAAACGACTAAAAAAGCAGCTTCaTCACTTAAAGA
 AAGTGATGTTTGGAGAATTTACCAGCTGTCAAAAAAGGGCACATCATAG
 AAAGTAACACGACGTGTTTTATTCTCTGACCCTCTATCTTTAGAAGCT
 CAATTAAATCATTTACAAA

Table 86: Comparative Sequences relating to SAG1393

SEQ ID NO. 8605

STRAIN 18RS21

GAAGGCTTCACCTATTATGGA
 AAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACAC
 TGGGTATTTATTAAACTAGGTGTTAATGTTTCAAGTTACAGTTTAGACT
 TAGAAAAAGATAGCCCCGTTTTTGGTAAACAACCTGAAAGAAGCTAAAAAA
 TTAACGTCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAAT
 CATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAATTGCAC
 CAACCTTAGTTATTAAATATGGTGACAAAAATTATTTAgATaTGATGCCA
 GCCTTGGGGAAAGTATTTCGGTAAAGAAAAgAAGCTAATCAGTGGGTTAG
 CCAATGGAAAACTAAAACTCTCGCTGTCAAAAAAGATTACACCATATCT
 TAAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAAATATC
 TATTTATATGGTAATAATTTTGGACGCGGTGGAGAATAATCTATGATTCT
 ACTAGGTTATGCTGCCCCagAAAAAGTCAAAAAgATGTCTTTAAAAAAG
 GGTGGTTTACCGTTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTAT
 GCCCTTGTTAATATAAAACAAACgACTAAAAAAGCAGCTTCATCACTTAA
 AGAAAGTGATGTCTGGAAGAATTACCAGCTGTCAAAAAAGGGCACATCA
 TAGAAAGTAACTACGACGTGTTTTATTCTCTGACCCTCTATCTTTAGAA
 GCTCAATTAAATCATTTACAAA

SEQ ID NO. 8606

STRAIN M732

GAAGGCTTCACCTATTATGG
 AAAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACA
 CTGGGTATTTATTAAACTAGGTGTTAATGTTTCAAGTTACAGTTTAGAC
 TTAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAA
 ATTAACGTCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTAA
 TCATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAATTGCA
 CCAACCTTAGTTATTAAATATGGTGACAAAAATTATTTAgATaTGATGCC
 AGCCTTGGGGAAAGTATTTCGGTAAAGAAAAAGAGCTAATCAGTGGGTTA
 GCCAATGGAAAACTAAAACTCTCGCTGCCAAAAAAGATTACACCATATC
 TTAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAAATAT
 CTATTTATATGGTAATAATTTTGGACgCGGTGGAGAACTAATCTATGATT
 CACTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAA
 GGGTGGTTTACCGTTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTA
 TGCCCTTGTTAATATAAAACAAACGACTAAAAAAGCAGCTTCATCACTTA
 AAGAAAGTGATGTCTGGAAGAATTACCAGCTGTCAAAAAAGGGCACATC
 ATAGAAAGTAACTACGACGTGTTTTATTCTCTGACCCTCTATCTTTAGA
 AGCTCAATTAAATCATTTACAAA

SEQ ID NO. 8607

STRAIN COH1

GAAGGCTTCACCTATTATG
 GAAAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTAC
 ACTGGGTATTTATTAAACTAGGTGTTAATGTTTCAAGTTACAGTTTAgA
 CTTAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAA
 AATTAACGTCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTAA
 ATCATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAATTGC
 ACCAATTTAGTTATTAAATATGGTGACAAAAATTATTTAgATaTGATGC
 CAGCCTTGGGGAAAGTaTTcGGTAAAGAAAAAGAGCTAATCAGTGGGTT
 AGCCAATGGAAAACTAAAACTCTCGCTGCCAAAAAAGATTTACACCATAT
 CTTAAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAAATA
 TCTATTTATATGGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGAT
 TCCTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAA
 AGGGTGGTTTTACCGTTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATT
 ATGCCCTTGTTAATATAAAACAAACGACTAAAAAAGCAGCTTCATCACTT
 AAAGAAAGTGATGTCTGGAAGAATTACCAGCTGTCAAAAAAGGGCACAT
 CATAGAAAGTAACTACGACGTGTTTTATTCTCTGACCCTCTATCTTTAG
 AAGCTCAATTAAATCATTTACAAA

SEQ ID NO. 8608

STRAIN M781

GAAGGCTTCACCTATTATGG
 AAAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACA
 CTGGGTATTTATTAAACTAGGTGTTAATGTTTCAAGTTACAGTTTAGAC
 TTAgAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAA
 ATTAACGTCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTAA
 TCATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAATTGCA
 CCAACCTTAGTTATTAAATATGGTGACAAAAATTATTTAgATaTGATGCC
 AGCCTTGGGGAAAGTATTTCGGTAAAGAAAAAGAGCTAATCAGTGGGTTA
 GCCAATGGAAAACTAAAACTCTCGCTGCCAAAAAAGATTTACACCATATC
 TTAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAAATAT
 CTATTTATATGGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGATT
 CACTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAA
 GGGTGGTTTACCGTTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTA
 TGCCCTTGTTAATATAAAACAAACGACTAAAAAAGCAGCTTCATCACTTA

Table 86: Comparative Sequences relating to SAG1393

AAGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAGGGCACATC
 ATAGAAAGTAACACGACGTGTTTATTCTCTGACCCCTCTATCTTTAGAA
 AGCTCAATTAATAATCATTACAAA

SEQ ID NO. 8609

STRAIN CJB110

GAAGGCTTCACCTATTATGGA
 AAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACAC
 TGGGTATTTATTAATACTAGGTGTTAATGTTTCAAGTTACAGTTTAGACT
 TAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAAA
 TTAACGTCTGATGATACAGAAGCTATTGCCGCACAAAACCTGATTTAAT
 CATGGTTTTCTGATCAAGATCCAAACATCAATACTCTGAAAAAATTGCAC
 CAACTTTAGTTATTAATATGGTGCACAAAATTTTAgATATGATGCCA
 GCCTTGGGGAAGTATTTCGGTAAAGAAAAAGAGCTAATCAGTGGGTAG
 CCAATGGAAAACTAAACTCTCGCTGCCAAAAAGATTACACCATATCT
 TAAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAATATC
 TATTTATATGTTAATAATTTTGGACGCGGTGGAGAACTAATCTATGATTC
 ACTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAGATGCTTTAAAAAAG
 GGTGGTTTACCGTTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTAT
 GCCCTTGTTAATATAACAAAACGACTAAAAAAGCAGCTTCATCACTTAA
 AGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAGGGCACATCA
 TAGAAAGTAACACGACGTGTTTATTCTCTGACCCCTCTATCTTTAGAA
 GCTCAATTAATAATCATTACAAA

SEQ ID NO. 8610

STRAIN 1169NT

GAAGGCTTCACCTATTATGGAATAAT
 CCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACACTGGGTA
 TTTATTAATACTAGGTGTTAATGTTTCAAGTTACAGTTTAGACTTAGAAA
 AAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAAATTAACT
 GCTGATGATACAGAAGCTATTGCCGcACAAAaACCTGATTTAATCATGGT
 TTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAATTGCACCAACTT
 TAGTTATTAATAATATGGTGCACAAAATTTTAgATATGATGCCAGCCTTG
 GGGAAAGTATTTCGGTAAAGAAAAAGGAACTAATCAGTGGGTAGCCAATG
 GAAAACTAAACTCTCGCTGCCAAAAAGATTACACCATATCTTAAAGC
 CTAACACTACTTTTACTATTATGGATTTTTATGATAAAAATATCTATTTA
 TATGGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGATTCAC TAGG
 TTATGCTGCCCCAgAAAAAGTCAAAAAGATGCTTTAAAAAAGGGTGGT
 TTACCGTTTTcGCAAGAAGCAATCGGTGATTACGTTGGAGATTATGCCCTT
 GTTAATATAAACAACGACTAAAAAAGCAGCTTCATCACTTAAAGAAAG
 TGATGTCTGGAAGAATTTACCAGCTGTCAAAAAGGGCACATCATAGAAA
 GTAACACGACGTGTTTATTCTCTGACCCCTCTATCTTTAGAAGCTCAA
 TTAAATCATTACAAA

SEQ ID NO. 8611

STRAIN JM9130013

GAAGGCTTCACCTATTATG
 GAAAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTAC
 ACTGATATTATTAAAACTAGGAGTTAATGTTTCAAGTTACAGTTTAGA
 CTTAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGGAGCTAAAA
 AATTAACTGCTGATGATACAGAAGCTATTGCCGCACAAAACCTGATTTA
 ATCATGGTTTTTATCAAGATCCAAACATCAATACTCTGAAAAAATTGTC
 ACCAATTTAGTTATTAAATATGGTGCACAAAATTTTAgATATGATGC
 CAGCTTTGGGGAAGTATTTCGGTAAAGAAAAAGAGCTAATCAGTGGGT
 AGCCAATGGAAAACTAAACTCTCGCTGCCAAAAAGATTACACCATAT
 CTTAAACCTAACACTACTTTTACCATTATGGATTTTTATGATAAAAATA
 TCTATTTATATGGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGAT
 TCCTAGGTTATGCTGCCCCAgAAAAAGTCAAAAAGATGCTTTAAAAA
 AGGGTGGTTTTACCGTTTTcGCAAGAAGCAATCGGTGATTACGTTGGAGATT
 ATGCCCTTGTTAATATAAACAACGACTAAAAAAGCAGCTTCATCACTT
 AAAGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAGGGCACAT
 CATAGAAAGTAACACGACGTGTTTTATTCTCTGACCCCTCTATCTTTAG
 AAGCTCAATTAATAATCATTACAAA

PRETTY of: /biotmp/msa521731.2{*} April 28, 2003 08:07 ..

	1	50
msa521731.2{691_090}	-----	-----
msa521731.2{691_1169NT}	-----	-----
msa521731.2{691_CJB110}	-----	-----
msa521731.2{691_COH1}	-----	-----
msa521731.2{691_M732}	-----	-----
msa521731.2{691_M781}	-----	-----
msa521731.2{691_18RS21}	-----	-----
msa521731.2{691_2603}	atgaaaaaaa	ttggaattat tgtcctcaca ctactgacct tctttttggt

Table 86: Comparative Sequences relating to SAG1393

msa521731.2{691_A909}	-----	-----	-----	-----	-----
msa521731.2{691_JM9130013}	-----	-----	-----	-----	-----
msa521731.2{691_H36B}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
msa521731.2{691_090}	51	-----	-----	-----	100
msa521731.2{691_1169NT}	-----	-----	-----	-----	-----
msa521731.2{691_CJB110}	-----	-----	-----	-----	-----
msa521731.2{691_COH1}	-----	-----	-----	-----	-----
msa521731.2{691_M732}	-----	-----	-----	-----	-----
msa521731.2{691_M781}	-----	-----	-----	-----	-----
msa521731.2{691_18RS21}	-----	-----	-----	-----	-----
msa521731.2{691_2603}	atcttgcgga	caacaaacta	aacaagaaag	cactaaaaca	actatttcta
msa521731.2{691_A909}	-----	-----	-----	-----	-----
msa521731.2{691_JM9130013}	-----	-----	-----	-----	-----
msa521731.2{691_H36B}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
msa521731.2{691_090}	101	-----	-----	-----	150
msa521731.2{691_1169NT}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_CJB110}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_COH1}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_M732}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_M781}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_18RS21}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_2603}	aaatgcctaa	aattGAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_A909}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_JM9130013}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_H36B}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
Consensus	*****	*****	*****	*****	*****
msa521731.2{691_090}	151	-----	-----	-----	200
msa521731.2{691_1169NT}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_CJB110}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_COH1}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_M732}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_M781}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_18RS21}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_2603}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_A909}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_JM9130013}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_H36B}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
Consensus	*****	*****	*****	*****	*****
msa521731.2{691_090}	201	-----	-----	-----	250
msa521731.2{691_1169NT}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_CJB110}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_COH1}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_M732}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_M781}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_18RS21}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_2603}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_A909}	ACTAGGaGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_JM9130013}	ACTAGGaGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_H36B}	ACTAGGaGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
Consensus	*****	*****	*****	*****	*****
msa521731.2{691_090}	251	-----	-----	-----	300
msa521731.2{691_1169NT}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_CJB110}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_COH1}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_M732}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_M781}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_18RS21}	CCGTTTTTGG	TAAaCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_2603}	CCGTTTTTGG	TAAaCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_A909}	CCGTTTTTGG	TAAaCAACTG	AAAGgAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_JM9130013}	CCGTTTTTGG	TAAgCAACTG	AAAGgAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_H36B}	CCGTTTTTGG	TAAgCAACTG	AAAGgAGCTA	AAAAATTAAC	TGCTGATGAT
Consensus	*****	***-*****	*****	*****	*****
msa521731.2{691_090}	301	-----	-----	-----	350
msa521731.2{691_1169NT}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_1169NT}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA

Table 86: Comparative Sequences relating to SAG1393

msa521731.2{691_CJB110}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_COH1}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_M732}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_M781}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_18RS21}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_2603}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_A909}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_JM9130013}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_H36B}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
Consensus	*****	*****	*****	*****	*****
msa521731.2{691_090}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_1169NT}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_CJB110}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_COH1}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_M732}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_M781}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_18RS21}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_2603}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_A909}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_JM9130013}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_H36B}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
Consensus	*****	*****	*****	*****	*****
msa521731.2{691_090}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_1169NT}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_CJB110}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_COH1}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_M732}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_M781}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_18RS21}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_2603}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_A909}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_JM9130013}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_H36B}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
Consensus	*****	*****	*****	*****	*****
msa521731.2{691_090}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_1169NT}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_CJB110}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_COH1}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_M732}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_M781}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_18RS21}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_2603}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_A909}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_JM9130013}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_H36B}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
Consensus	*****	*****	*****	*****	*****
msa521731.2{691_090}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_1169NT}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_CJB110}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_COH1}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_M732}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_M781}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_18RS21}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_2603}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_A909}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_JM9130013}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_H36B}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
Consensus	*****	*****	*****	*****	*****
msa521731.2{691_090}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_1169NT}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_CJB110}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_COH1}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_M732}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_M781}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_18RS21}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_2603}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_A909}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_JM9130013}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT

Table 86: Comparative Sequences relating to SAG1393

msa521731.2{691_H36B}	CTTTTACTAT	TATaGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
Consensus	*****_**	***-*****	*****	*****	*****
	601				650
msa521731.2{691_090}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_1169NT}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_CJB110}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_COH1}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_M732}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_M781}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_18RS21}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_2603}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_A909}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_JM9130013}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_H36B}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
Consensus	*****	*****	*****	*****	*****
	651				700
msa521731.2{691_090}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_1169NT}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_CJB110}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_COH1}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_M732}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_M781}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_18RS21}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_2603}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_A909}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_JM9130013}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_H36B}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
Consensus	*****	*****	*****	*****	*****
	701				750
msa521731.2{691_090}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_1169NT}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_CJB110}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_COH1}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_M732}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_M781}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_18RS21}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_2603}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_A909}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_JM9130013}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_H36B}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
Consensus	*****	*****	*****	*****	*****
	751				800
msa521731.2{691_090}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_1169NT}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_CJB110}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_COH1}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_M732}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_M781}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_18RS21}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_2603}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_A909}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_JM9130013}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_H36B}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
Consensus	*****	*****	*****	*****	*****_**
	801				850
msa521731.2{691_090}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_1169NT}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_CJB110}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_COH1}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_M732}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_M781}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_18RS21}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_2603}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_A909}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_JM9130013}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_H36B}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
Consensus	*****	*****	*****	*****	*****
	851				900
msa521731.2{691_090}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_1169NT}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_CJB110}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_COH1}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA

Table 86: Comparative Sequences relating to SAG1393

msa521731.2{691_M732}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_M781}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_18RS21}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_2603}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_A909}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_JM9130013}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_H36B}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
Consensus	*****	*****	*****	*****	*****

	901		930
msa521731.2{691_090}	TTTACAAA--	-----	-----
msa521731.2{691_1169NT}	TTTACAAA--	-----	-----
msa521731.2{691_CJB110}	TTTACAAA--	-----	-----
msa521731.2{691_COH1}	TTTACAAA--	-----	-----
msa521731.2{691_M732}	TTTACAAA--	-----	-----
msa521731.2{691_M781}	TTTACAAA--	-----	-----
msa521731.2{691_18RS21}	TTTACAAA--	-----	-----
msa521731.2{691_2603}	TTTACAAAgg	ctatcaaaga	aaatacaaat
msa521731.2{691_A909}	TTTACAAA--	-----	-----
msa521731.2{691_JM9130013}	TTTACAAA--	-----	-----
msa521731.2{691_H36B}	TTTACAAA--	-----	-----
Consensus	*****	*****	*****

SEQ ID NO. 8612

STRAIN 2603 frame: 1

MKKIGIIVLTLLTFFLVSCGQQTKESTKTTISKMPKIEGFTYYGKIPENPKKVINFTYS
 YTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLTADDTEAIAAQKPDLMVFDQDPN
 INTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEANQWVSQWKTTLAVKKDLHHILK
 PNTTFTIMDFYDKNIYLYGNNGFRGGELIYDSLGYAAPEKVKKDVFKKGWFTVSQEAIGD
 YVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHIIESNYDVFFYFSDPLSLEAQLKS
 FTKAIKENTN

SEQ ID NO. 8613

STRAIN 090 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEAN
 QWVSQWKTTLAAKDLHHILKPNNTTFTIMDFYDKNIYLYGNNGFRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8614

STRAIN A909 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEAN
 QWVSQWKTTLAAKDLHHILKPNNTTFTIMDFYDKNIYLYGNNGFRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8615

STRAIN H36B frame: 1

EGFTYYGKIPENPKKVINFTYSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEAN
 QWVSQWKTTLAAKDLHHILKPNNTTFTIDFYDKNIYLYGNNGFRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8616

STRAIN 18RS21 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEAN
 QWVSQWKTTLAAKDLHHILKPNNTTFTIMDFYDKNIYLYGNNGFRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8617

STRAIN M732 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEAN
 QWVSQWKTTLAAKDLHHILKPNNTTFTIMDFYDKNIYLYGNNGFRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8618

STRAIN COH1 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEAN

Table 86: Comparative Sequences relating to SAG1393

QWVSQWKTTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8619

STRAIN M781 frame: 1

EGFTYYGKIPENPKKVINFYTSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLTA
 DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMMPALGKVFGKEKEAN
 QWVSQWKTTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8620

STRAIN CJB110 frame: 1

EGFTYYGKIPENPKKVINFYTSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLTA
 DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMMPALGKVFGKEKEAN
 QWVSQWKTTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8621

STRAIN 1169NT frame: 1

EGFTYYGKIPENPKKVINFYTSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLTA
 DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMMPALGKVFGKEKEAN
 QWVSQWKTTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8622

STRAIN JM9130013 frame: 1

EGFTYYGKIPENPKKVINFYTSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLTA
 DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMMPALGKVFGKEKEAN
 QWVSQWKTTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

PRETTY of: /biotmp/msa522124.2{*} April 28, 2003 08:17 ..

	1				50
msa522124.2{691_090}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_1169NT}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_CJB110}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_COH1}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_M732}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_M781}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_18RS21}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_2603}	mkkigiivlt	lltfflvscg	qqtqgestkt	tiskmpkieg	FTYYGKIPEN
msa522124.2{691_A909}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_JM9130013}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_H36B}	-----	-----	-----	-----	EG FTYYGKIPEN
Consensus	*****	*****	*****	*****	*****
	51				100
msa522124.2{691_090}	PKKVINFTYS	YTGYYLLKLG	NVSSYSLDLE	KDSPVFGKQL	KeAKKLTAADD
msa522124.2{691_1169NT}	PKKVINFTYS	YTGYYLLKLG	NVSSYSLDLE	KDSPVFGKQL	KeAKKLTAADD
msa522124.2{691_CJB110}	PKKVINFTYS	YTGYYLLKLG	NVSSYSLDLE	KDSPVFGKQL	KeAKKLTAADD
msa522124.2{691_COH1}	PKKVINFTYS	YTGYYLLKLG	NVSSYSLDLE	KDSPVFGKQL	KeAKKLTAADD
msa522124.2{691_M732}	PKKVINFTYS	YTGYYLLKLG	NVSSYSLDLE	KDSPVFGKQL	KeAKKLTAADD
msa522124.2{691_M781}	PKKVINFTYS	YTGYYLLKLG	NVSSYSLDLE	KDSPVFGKQL	KeAKKLTAADD
msa522124.2{691_18RS21}	PKKVINFTYS	YTGYYLLKLG	NVSSYSLDLE	KDSPVFGKQL	KeAKKLTAADD
msa522124.2{691_2603}	PKKVINFTYS	YTGYYLLKLG	NVSSYSLDLE	KDSPVFGKQL	KeAKKLTAADD
msa522124.2{691_A909}	PKKVINFTYS	YTGYYLLKLG	NVSSYSLDLE	KDSPVFGKQL	KgAKKLTAADD
msa522124.2{691_JM9130013}	PKKVINFTYS	YTGYYLLKLG	NVSSYSLDLE	KDSPVFGKQL	KgAKKLTAADD
msa522124.2{691_H36B}	PKKVINFTYS	YTGYYLLKLG	NVSSYSLDLE	KDSPVFGKQL	KgAKKLTAADD
Consensus	*****	*****	*****	*****	*-*****
	101				150
msa522124.2{691_090}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_1169NT}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_CJB110}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_COH1}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_M732}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_M781}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_18RS21}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_2603}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_A909}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_JM9130013}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV

Table 86: Comparative Sequences relating to SAG1393

msa522124.2{691_H36B}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
Consensus	*****	*****	*****	*****	*****
	151				200
msa522124.2{691_090}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_1169NT}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_CJB110}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_COH1}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_M732}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_M781}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_18RS21}	FGKEKEANQW	VSQWKTKTTLA	vKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_2603}	FGKEKEANQW	VSQWKTKTTLA	vKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_A909}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_JM9130013}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_H36B}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
Consensus	*****	*****	*****	*****	*****
	201				250
msa522124.2{691_090}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_1169NT}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_CJB110}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_COH1}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_M732}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_M781}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_18RS21}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_2603}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_A909}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_JM9130013}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_H36B}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
Consensus	*****	*****	*****	*****	*****
	251				300
msa522124.2{691_090}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVFFYFSD	PLSLEAQLKS
msa522124.2{691_1169NT}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVFFYFSD	PLSLEAQLKS
msa522124.2{691_CJB110}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVFFYFSD	PLSLEAQLKS
msa522124.2{691_COH1}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVFFYFSD	PLSLEAQLKS
msa522124.2{691_M732}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVFFYFSD	PLSLEAQLKS
msa522124.2{691_M781}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVFFYFSD	PLSLEAQLKS
msa522124.2{691_18RS21}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVFFYFSD	PLSLEAQLKS
msa522124.2{691_2603}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVFFYFSD	PLSLEAQLKS
msa522124.2{691_A909}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVFFYFSD	PLSLEAQLKS
msa522124.2{691_JM9130013}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVFFYFSD	PLSLEAQLKS
msa522124.2{691_H36B}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVFFYFSD	PLSLEAQLKS
Consensus	*****	*****	*****	*****	*****
	301	310			
msa522124.2{691_090}	FT-----				
msa522124.2{691_1169NT}	FT-----				
msa522124.2{691_CJB110}	FT-----				
msa522124.2{691_COH1}	FT-----				
msa522124.2{691_M732}	FT-----				
msa522124.2{691_M781}	FT-----				
msa522124.2{691_18RS21}	FT-----				
msa522124.2{691_2603}	FTkaikentn				
msa522124.2{691_A909}	FT-----				
msa522124.2{691_JM9130013}	FT-----				
msa522124.2{691_H36B}	FT-----				
Consensus	*****				

Table 87: Comparative Sequences relating to SAG0645

SEQ ID NO. 8701

STRAIN 2603

ATGAAATATCGAAGAAGTTATTGTTTTTCGGCTGCTGTT
 TTAACAATGGTGGCGGGTCAACTGTTGAACCAAGTAGCTCAGTTTGGCGACTGGAATGAGT
 ATTGTAAGAGCTGCAGAAGTGTCAAGAAGCGCCAGCGAAAAACAACAGTAAATATCTAT
 AAATTACAAGCTGATAGTTATAAATCGGAAATTACTTCTAATGGTGGTATCGAGAATAAA
 GACGGCGAAGTAATATCTAACTAGCTAACTTGGTGACAATGTAAAAGGTTTGCAAGGT
 GTACAGTTTAAACGTTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTG
 ACAACAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTGAGTCTA
 CCTCAAAAACTAATGCTCAAGGTTTGGTCGTGATGCTCTGGATTCAAAAAAGTAATGTG
 AGATACCTTGTATGTAGAAGATTTAAAGAATTACCTTCAAACATTACCAAGCTTATGCT
 GTACCGTTTGTGTTGGAATTACCAGTTGCTAACTCTACAGGTACAGGTTTCCCTTCTGAA
 ATTAATATTTACCCTAAAAACGTTGTAACCTGATGAACCAAAACAGATAAAGATGTTAAA
 AAATTAGGTGACGACGATGACAGGTTATACGATTGGTGAAGAATTCAAATGGTTCTTGAAA
 TCTACAATCCCTGCCAATTAGGTGACTATGAAAAATTGAAATTAAGTATAAATTTGCA
 GATGGCTTGACTTATAAATCTGTTGGAATAATCAAGATTGGTTGAAAAACACTGAATAGA
 GATGAGCACTACACTATTGATGAACCAACAGTTGATAACCAAAATACATTAATAATTACG
 TTTAAACCAGAGAAATTTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCTTGTTTAAA
 AATCAAGATGCTCTTGTATAAAGCTACTGCAAAATACAGATGATGCGGCATTTTGGAAATT
 CCAAGTTGCTCAACTATTATGAAAAAGCAGTTTAGGAAAGCAATTGAAAAATCTTTT
 GAACCTTCAATATGACCAATCTCCTGATAAAGCTGACAAATCCAAACCACTAATCCTCCA
 AGAAACAGAGAGTTTCACTGTTGGGAAACGATTGTAAGAAAGACTCAACAGAAACA
 CAAACACTAGGTGGTCTGAGTTTGAATTTGTTGGCTTCTGATGGGACAGCAGTAAATGG
 ACAGATGCTCTTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGTTACT
 GGGCAACCAATCAAAATTGAAATCACATACAGACGGTACGTTTGAAGTTAAAGGTTTGGCT
 TATGCAAGTTGATGCGAATGACAGGGTACAGCAGTAACCTACAAATTTAAAGAAACAAAA
 GCACCAGAAGGTTATGTAATCCCTGATAAAGAAATCGAGTTTACAGTATCACAAACATCT
 TATAATACAAACCACTGACATCACGGTTGATAGTCTGATGCAACCTGATACAAATT
 AAAAACCAACCAACCTCCTTCAATCCCTAATACTGGTGGTATGGTACGGCTATCTTTGTC
 GCTATCGGTGCTGCGGTGATGGCTTTTGTGTTAAGGGGATGAAGCGTCTACAAAGAT
 AAC

SEQ ID NO. 8702

STRAIN 090

GCAGAAGTGTCAAGAAGCGCCAGCGAAAAAC
 AGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
 CTTCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTAT
 GCTAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAACG
 TTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAA
 CAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTC
 AGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTGATGCTCTGGA
 TTTCAAAAAGTAAATGTGAGATACCTGATGTAGAAGATTAAAGAATTAC
 CTTCAAAACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCA
 GTTGCTAACTCTACAGGTACAGGTTTCTTTCTGAAATTAATATTACCC
 TAAAAACGTTGTAACCTGATGAACCAAAACAGATAAAGATGTTAAAAAAT
 TAGGTGAGACGATGACAGGTTATACGATTGGTGAAGAATTCAAATGGTTCT
 TTGAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTGAAAT
 TACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAATAATCA
 AGATTGGTTGAAAAACACTGAATAGAGATGAGCACTACACTATTGATGAA
 CCAACAGTTGATAACCAAAATACATTAATAAATTACGTTTAAACCCAGAGAA
 ATTTAAAGAAATTTGCTGAGCTACTTAAAGGAATGACCTTGTAAAAAATC
 AAGATGCTCTTGATAAAGCTACTGCAAAATACAGATGATGCGGCATTTTGG
 GAAATTCAGTTGCTACACTATTAAATGAAAAAGCAGTTTGGGAAAAAGC
 AATTGAAAAATCTTTTGAACCTTCAATATGACCATACCTGATAAAGCTG
 ACAATCCAAAACCATCTAATCCTCCAAAGAAACAGAAAGTTTCACTAGGT
 GGGAAACGATTGTAAGAAAGACTCAACAGAAACACAAACACTAGGTGG
 TGCTGAGTTTGATTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAG
 ATGCTCTTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCT
 GTTACTGGGCAACCAATCAAATGAAATCACATACAGACGGTACGTTTGA
 GATTAAAGGTTTGGCTTATGCAAGTTGATGCGAATGCAGAGGTTACAGCAG
 TAACTTACAAATTTAAAGAAACAAAGCACCAGAAGGTTATGTAATCCCT
 GATAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAACCC
 AACTGACATCACGGTTGATAGTGTGATGCAACACCTGATACAAATTAATA
 ACAACAAACGTCCTTCA

SEQ ID NO. 8703

STRAIN A909

GCAGAAGTGTCAAGAAGCGCCAGCGAA
 AACCAACAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAA
 TTACTTCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAAC
 TATGCTAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAA
 ACGTTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGA
 CAACAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGT
 GTCAAGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTGATGCTCT
 GGAATCAAAAAGTAAATGTGAGATACCTGATGTAGAAGATTAAAGAATT
 CACCTTCAAAACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTA
 CCAGTTGCTAACTCTACAGGTACAGGTTTCTTTCTGAAATTAATATTTA
 CCCTAAaAACGTTGTAACCTGATGAACCAAAACAGATAAAGATGTTAAAA
 AATTAGGTGACGACGATGACAGGTTATACGATTGGTGAAGAATTCAAATGG
 TTCTTGAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTGGA
 AATTACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAATAA
 TCAAGATTGGTTGAAAAACACTGAATAGAGATGAGCACTACACTATTGAT
 GAACCAACAGTTGATAACCAAAATACATTAAAAATTACGTTTAAACCGA

Table 87: Comparative Sequences relating to SAG0645

GAAATTTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCCCTTGTTAAAA
 ATCAAGATGCTCTTGATAAAGCTACTGCAATACAGATGATGCGGCATTT
 TTGGAAATTCAGTTGTCATCAACTATTAATGAAAAAGCAGTTTATAGGAAA
 AGCAATTGAAAACTCTTTGAACTTCAATATGACCATACTCCTGATAAAG
 CTGACAAATCCAAAACCATCTAATCCTCCAGAAAACCCAGAAAGTTCATACT
 GGTGGGAAACGATTTGTAAGAAAAGACTCAACAGAAAACAAAACACTAGG
 TGGTGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAATGGGA
 CAGATGCTCTTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAA
 GCTGTACTGTTGGGCAACCAATCAAATGAAATCACAATACAGACGGTACGTT
 TGAGATTAAAGGTTTGGCTTATGCAAGTTGATGCGAATGCAGAGGGTACAG
 CAGTAACCTTACAAATTAAAAAGAAAACAAAGCACCAGAGGTTATGTAATC
 CCTGATAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAA
 ACCAACTGACATCACGGTTGATAGTCTGATGCAACACCTGATACAAATTA
 AAAACAACAA

SEQ ID NO. 8704

STRAIN 18RS21

GCAGAAGTGTCAAGAAGCGCCAGCGAAAAAC
 AGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
 CTCTTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTAT
 GCTAAACTTGGTGACAATGTAAGAGGTTTGCAAGGTGTACAGTTTAAACG
 TTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAA
 CAGTTGAAGCAGCAGATGCAAAAGTTGGAAACGATCTTGAAGAAGGTGTC
 AGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGA
 TTCAAAAGTAATGTGAGATACTTGTATGTAGAAGATTAAAGAATTTCAC
 CTTCAAACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCA
 GTTGCTAACTCTACAGGTACAGGTTTCTTTCTGAAATTAATATTACCC
 TAAAAACGTTGTAAGTATGAACCAAAAAACAGATAAAGATGTTAAATAAT
 TAGGTACAGACGATGCAAGGTTATACGATTGGTGAAGAATTCAAATGGTTC
 TTGAATCTACAATCCCTGCCAATTAGGTGACTATGAAAAATTTGAAAT
 TACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGAAAAATCA
 AGATTGGTTGAAAAACCTGAATAGAGATGAGCACTACACTATTGATGAA
 CCAACAGTTGATAACCAAAATACATTAAAAAATTACGTTTAAACCAAGAGAA
 ATTTAAAGAAATTTGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAAATC
 AAGATGCTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTTTGTG
 GAAATTCAGTTGCATCAACTATTAAATGAAAAAGCAGTTTATAGGAAAAGC
 AATTGAAAAATCTTTTGAACCTCAATATGACCACTACTCTGATCAAGCTG
 ACAATCCAAACCATCTAATCCTCCAGAAAACCCAGAAAGTTCATACTGGT
 GGGAAACGATTTGTAAGAAAAGACTCAACAGAAAACAAAACACTAGGTGG
 TGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAG
 ATGCTCTTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCT
 GTTACTGGGCAACCAATCAAATTTGAAATCACAATACAGACGGTACGTTTGA
 GATTAAAGGTTTGGCTTATGCAAGTTGATGCGAATGCAGAGGGTACAGCAG
 TAACCTTACAAATTTAAAGAAAACAAAGCACCAGAGGTTATGTAATCCCT
 GATAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAAAC
 AACTGACATCACGGTTGATAGTCTGATGCAACACCTGATACAAATTA
 ACAACAAACGTCCTTCA

SEQ ID NO. 8705

STRAIN M732

GCAGAAGTGTCAAGAAGCGCCAGCGAAAAACACAGT
 AAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTAATCTTA
 ATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGCTAAA
 CTGTTGAGCAATGTAAGAGGTTTGCAAGGTGTACAGTTTAAACGTTATAA
 AGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAACAGTGTG
 AAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTGAGTCTA
 CCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGATTCAAA
 AAGTAATGTGAGATACTTGTATGTAGAAGATTAAAGAATTACCTTCAA
 ACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTACAGTTGCT
 AACTCTACAGGTACAGGTTTCTTTCTGAAATTAATATTACCTAAAAA
 CGTTGTAACTGATGAACCAAAAAACAGATAAAGATGTTAAAAAATTAGGTC
 AGGACGATGCAAGTTATACGATTTGGTGAAGAATTCAAATGGTTCTTGAA
 TCTACAATCCCTGCCAATTTAGGTGACTATGAAAAAATTGAAATTACTGA
 TAAATTTGCAGATGGCTTGACTTATAAATCTGTTGAAAAAATCAAGATTG
 GTTCGAAAACTGAATAGAGATGAGCACTACACTATTGATGAACCAACA
 GTTGATAACCAAAATACATTAAAAATTACGTTTAAACCAAGAGAAATTA
 AGAAATTTGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAAATCAAGATG
 CTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTTTGGAAATT
 CCAGTTGCATCAACTATTAATGAAAAAGCAGTTTATAGGAAAAGCAATTGA
 AAATACTTTTGAACCTCAATATGACCATACTCTGATAAAGCTGACAATC
 CAAAACCACTAATCTCCAGAAAACCCAGAAAGTTCATACTGGTGGGAAA
 CGATTGTAAAGAAAGACTCAACAGAAAACAAAACACTAGGTGGTGTGTA
 GTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAGATGCTC
 TTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGTTACT
 GGGCAACCAATCAAATTTGAAATCACAATACAGACGGTACGTTTGAATTA
 AGGTTTGGCTTATGCAAGTTGATGCGAATGCAGAGGGTACAGCAGTAACCT
 ACAATTTAAAGAAAACAAAGCACCAGAGGTTATGTAATCCCTGATAAA
 GAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAAACCACTGA
 CATCACGGTTGATAGTCTGATGCAACACCTGATACAAATTA
 AACGTCCTTCA

SEQ ID NO. 8706

STRAIN COHI

Table 87: Comparative Sequences relating to SAG0645

GCAGAAGTGTCAAGAAGCGCCAGCGAAAAC
 AGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
 CTTnTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTAT
 GCTAAACTTGGTGACAATGTAAAGGTTTGCAGGTGTACAGTTTAAACG
 TTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAA
 CAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTC
 AGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGA
 TTCAAAAAGTAAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTCAC
 CTTCAAAACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCA
 GTTGCTAACTCTACAGGTACAGGTTTCCTTTCTGAAATTAATATTACCC
 TAAAAACGTTGTAACGTGATGAACCAAAACAGATAAAGATGTTAAAAAAT
 TAGGTGAGGACGATGACAGTTATACGATTGGTGAAGAATTCAAATGGTTC
 TTGAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAAATTGAAAT
 TACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAATAATCA
 AGATTGGTTGCAAAACACTGAATAGAGATGAGCACTACACTATTGATGAA
 CCAACAGTTGATAACCAAAATACATTAAAAATTACGTTTAAACAGAGAA
 ATTTAAAGAAATGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAAATC
 AAGATGCTCTTGATAAAGCTACTGCAATACAGATGATGCGGCATTTTGTG
 GAAATTCAGTTGCATCAACTATTAAATGAAAAAGCAGTTTTAGGAAAAGC
 AATTGAAAAATACTTTGAACCTCAATATGACCATACTCCTGATAAAGCTG
 ACAATCCAAACCACTCTAATCCTCCAAGAAAACCAAGAAGTTCACTAGGT
 GGGAAACGATTTGTAAGAAAGACTCAACAGAAACACAAACACTAGGTGG
 TGCAGGTTTGTATTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAG
 ATGCTCTTATTAAGCGAATACTAATAAAAACTATATTGCTGGAGAGCT
 GTTACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGA
 GATTAAGGTTTGGCTTATGCAAGTTGATGCGAATGCAGAGGGTACAGCAG
 TAACCTTCAAAATTAAGAAACAAAAGCACCAGAAGGTTATGTAATCCCT
 GATAAAGAAATCGAGTTTACAGTATCAAAACATCTTATAATACAAAACC
 AACTGACATCACGGTTGATAGTGTGATGCAACACCTGATACAATTAATA
 ACAACAAACGTCCTTCA

SEQ ID NO. 8707

STRAIN M781

GCAGAAGTGTCAAGAAGCGCCAGCGAAAACAG
 CAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
 TCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGC
 TAAACCTTGGTGACAATGTAAAGGTTTGCAGGTGTACAGTTTAAACGTT
 ATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACACA
 GTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTCAG
 TCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGATT
 CAAAAAGTAAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTACCT
 TCAACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTACAGT
 TGCTAACTCTACAGGTACAGGTTTCCTTTCTGAAATTAATATTACCTTA
 AAAACGTTGTAACTGATGAACCAAAACAGATAAAGATGTTAAAAAATTA
 GGTCAAGACGATGCAAGTTTATACGATTGGTGAAGAATTCAAATGGTTCTT
 GAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTGAAATTA
 CTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAATAATCAAG
 ATTGGTTTCGAAAACACTGAATAGAGATGAGCACTACACTATTGATGAACC
 AACAGTTGATAACCAAAATACATTAAAAATTACGTTTAAACAGAGAAAT
 TTAAGAAATTTGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAAATCAA
 GATGCTCTTGATAAGCTACTGCAAAATACAGATGATGCGGCATTTTGGTA
 AATTCCAGTTGCACTCAACTATTAAATGAAAAAGCAGTTTTAGGAAAAGCAA
 TTGAAAAATCTTTTGAACCTTCAATATGACCATACTCCTGATAAAGCTGAC
 AATCCAAAACCACTAATCCTCCAAGAAAACCAAGAAGTTCACTAGGTGG
 GAAACGATTTGTAAGAAAGACTCAACAGAAACCAAAACACTAGGTGGTG
 CTGAGTTTGTATTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAGAT
 GCTCTTATTAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGT
 TACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGA
 TTAAGGTTTGGCTTATGCAAGTTGATGCGAATGCAGAGGGTACAGCAGTA
 ACTTACAAATTAAGAAACAAAAGCACCAGAAGGTTATGTAATCCCTGA
 TAAAGAAATCGAGTTTACAGTATCAAAACATCTTATAATACAAAACCAA
 CTGACATCACGGTTGATAGTGTGATGCAACACCTGATACAATTAATAAC
 AACAAACGT

SEQ ID NO. 8708

STRAIN CJB110

GCAGAAGTGTCAAGAAGCGCCAGCGAA
 AACAGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATGGAAA
 TTACTTCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAAC
 TATGCTAAACTTGGTGACAATGTAAAGGTTTGCAGGTGTACAGTTTAA
 ACGTTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGA
 CAACAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGT
 GTCAAGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCT
 GGATTCAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATT
 CACCTTCAAAACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTA
 CCAAGTTGCTAACTCTACAGGTACAGGTTTCCTTTCTGAAATTAATATT
 CCTTAAAAACGTTGTAATGATGAACCAAAACAGATAAAGATGTTAAAA
 AATTAGGTGAGGACGATGCAAGTTTATACGATTGGTGAAGAATTCAAATGG
 TCTTGAAGATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAAATTGA
 AATTACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAATA
 TCAAGATTGGTTGGAACCACTGAATAGAGATGAGCACTACACTATTGAT
 GAACCAACAGTTGATAACCAAAATACATTAAAAATTACGTTTAAACAGAA
 GAAATTTAAAGAAATTTGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAA

Table 87: Comparative Sequences relating to SAG0645

ATCAAGATGCTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTT
 TTGGAAATTCAGTTGTCATCAACTATTAATGAAAAAGCAGTTTATAGGAAA
 AGCAATTGAAAACTCTTTGAACTTCAATATGACCATACTCCTGATAAAG
 CTGCAATcCAAAACCATCTAATCCTCCAGAAAACAGAGTTCTACT
 GGTGGGAAACGATTTGTAAAGAAAGACTCAACAGAAAACACAAACACTAGG
 TGGTGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAATGGA
 CAGATGCTCTTATTAAGCGAATACTAATAAAAACTATATTGCTGGAGAA
 GCTGTTACTGGGCAACCAATCAAAATGAAATCACATACAGACGGTACGTT
 TGAGATTAAAGGTTTGGCTTATGCGAGTTGATGCGAATGCAGAGGGTACAG
 CAGTAACCTACAAATTAAAGAAAACAAAGCACCAGAGGTTATGTAATC
 CCTGATAAAGAAATCGAGTTTACAGTATCACAACATCTTATAATCCAAA
 ACCAATGACATCAGGTTGATAGTGCTGATGCAACCTGATACAATTA
 AAAACAACAAACGCTCCTCA

SEQ ID NO. 8709

STRAIN JM9130013

GCAGAAGTGTCAAGAACGCCAGCGAAAACAGCAGTA
 AATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACTTCTAA
 TGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAATGCTAAAC
 TTGGTGACAAATGTAAGGTTTGCAGGTTGATCAGTTTAAACGTTATAAA
 GTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAACAGTTGA
 AGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTCAGTCTAC
 CTCAAAAAATAATGCTCAAGGTTTGGTTCGTCGATGCTCTGGATTCAAAA
 AGTAATGTGAGATACCTGTATGTAGAAGATTTAAAGAATTACCTTCAAA
 CATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTACAGTTGCTA
 ACTCTACAGGTACAGGTTTCTTTCTGAATTAATATTACCTAAAAAC
 GTTGTAACTGATGAACCAAAAACAGATAAAGATGTTAAAAAATTAGGTCA
 GGACGATGCGAGTTATACGATTGGTGAAGAATTCAAAATGGTTCTTGAAAT
 CTACAATCCCTGCCAATTTAGGTGACTATGAAAAAATTGAAATTACTGAT
 AAATTTGAGATGGCTTGACTTATAAATCTGTTGGAATAATCAAGATTGG
 TTGAAAAACACTGAATAGAGATGAGCACTACACTATTGATGAACCAACAG
 TTGATAACCAAAATACATTAATAAATTACGTTTAAACAGAGAAATTTAAA
 GAAATTTGCTGAGCTACTTAAAGGAATGACCTTGTATAAATCAAGATGC
 TCTTGATAAAGCTACTGCAAAATACAGATGATGCGGCATTTTGGAAATTC
 CAGTTGCTCAACTATTAAATGAAAAAGCAGTTTATGGAAGAAGCAATTGAA
 AATACTTTTGAACCTCAATATGACCATACTCTGATAAAGCTGACAAATCC
 AAAACCATCTAATcCTcCAAGAAAACAGAAAGTTCATCTGTTGGGAAAC
 GATTTGTAAGAAAGACTCAACAGAAAACACAAACACTAGGTGGTGTCTGAG
 TTTGATTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAGATGCTCT
 TATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGTTACTG
 GGCACCAATCAAATTGAAATCACATACAGACGGTACGTTTGGAGATTAA
 GGTTTGGCTTATGCAAGTTGATGCGAATGCAGAGGGTACAGCAGTAACCTA
 CAAATTAAGAAAACAAAGCACCAGAGGTTATGTAATCCCTGATAAAG
 AAATCGAGTTTACAGTATCACAACATCTTATAATACAAAACCACTGAC
 ATCAGGTTGATAGTGCTGATGCAACCTGATACAATTAACAAACACAA
 ACGTCTCTCA

PRETTY of: /biotmp/msa123961.2{*} April 30, 2003 07:17 ..

	1				50
msa123961.2{80_2603}	atgaaattat	cgaagaagtt	attgtttttcg	gctgctgttt	taacaatggt
msa123961.2{80_A909}	-----	-----	-----	-----	-----
msa123961.2{80_M732}	-----	-----	-----	-----	-----
msa123961.2{80_090}	-----	-----	-----	-----	-----
msa123961.2{80_COH1}	-----	-----	-----	-----	-----
msa123961.2{80_M781}	-----	-----	-----	-----	-----
msa123961.2{801_JM9130013}	-----	-----	-----	-----	-----
msa123961.2{80_18RS21}	-----	-----	-----	-----	-----
msa123961.2{80h_CJB110}	-----	-----	-----	-----	-----
Consensus	-----	-----	-----	-----	-----

	51				100
msa123961.2{80_2603}	ggcgggggtca	actgttgaac	cagtagctca	gtttgcgact	ggaatgagta
msa123961.2{80_A909}	-----	-----	-----	-----	-----
msa123961.2{80_M732}	-----	-----	-----	-----	-----
msa123961.2{80_090}	-----	-----	-----	-----	-----
msa123961.2{80_COH1}	-----	-----	-----	-----	-----
msa123961.2{80_M781}	-----	-----	-----	-----	-----
msa123961.2{801_JM9130013}	-----	-----	-----	-----	-----
msa123961.2{80_18RS21}	-----	-----	-----	-----	-----
msa123961.2{80h_CJB110}	-----	-----	-----	-----	-----
Consensus	-----	-----	-----	-----	-----

	101				150
msa123961.2{80_2603}	ttgtaagagc	tGCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{80_A909}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{80_M732}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{80_090}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{80_COH1}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{80_M781}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{801_JM9130013}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{80_18RS21}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{80h_CJB110}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAgCAGTA		
Consensus	-----	-*****	*****	*****	*****		
msa123961.2{80_2603}	151	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTcTAA	200
msa123961.2{80_A909}		AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTcTAA	
msa123961.2{80_M732}		AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTcTAA	
msa123961.2{80_090}		AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTcTAA	
msa123961.2{80_COH1}		AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTcTAA	
msa123961.2{80_M781}		AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTcTAA	
msa123961.2{801_JM9130013}		AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTcTAA	
msa123961.2{80_18RS21}		AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTcTAA	
msa123961.2{80h_CJB110}		AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTcTAA	
Consensus		*****	*****	*****	*****	*****	
msa123961.2{80_2603}	201	TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC	250
msa123961.2{80_A909}		TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC	
msa123961.2{80_M732}		TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC	
msa123961.2{80_090}		TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC	
msa123961.2{80_COH1}		TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC	
msa123961.2{80_M781}		TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC	
msa123961.2{801_JM9130013}		TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC	
msa123961.2{80_18RS21}		TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC	
msa123961.2{80h_CJB110}		TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC	
Consensus		*****	*****	*****	*****	*****	
msa123961.2{80_2603}	251	TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA	300
msa123961.2{80_A909}		TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA	
msa123961.2{80_M732}		TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA	
msa123961.2{80_090}		TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA	
msa123961.2{80_COH1}		TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA	
msa123961.2{80_M781}		TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA	
msa123961.2{801_JM9130013}		TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA	
msa123961.2{80_18RS21}		TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA	
msa123961.2{80h_CJB110}		TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA	
Consensus		*****	*****	*****	*****	*****	
msa123961.2{80_2603}	301	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA	350
msa123961.2{80_A909}		GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA	
msa123961.2{80_M732}		GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA	
msa123961.2{80_090}		GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA	
msa123961.2{80_COH1}		GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA	
msa123961.2{80_M781}		GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA	
msa123961.2{801_JM9130013}		GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA	
msa123961.2{80_18RS21}		GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA	
msa123961.2{80h_CJB110}		GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA	
Consensus		*****	*****	*****	*****	*****	
msa123961.2{80_2603}	351	AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC	400
msa123961.2{80_A909}		AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC	
msa123961.2{80_M732}		AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC	
msa123961.2{80_090}		AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC	
msa123961.2{80_COH1}		AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC	
msa123961.2{80_M781}		AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC	
msa123961.2{801_JM9130013}		AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC	
msa123961.2{80_18RS21}		AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC	
msa123961.2{80h_CJB110}		AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC	
Consensus		*****	*****	*****	*****	*****	
msa123961.2{80_2603}	401	CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA	450
msa123961.2{80_A909}		CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA	
msa123961.2{80_M732}		CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA	
msa123961.2{80_090}		CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA	
msa123961.2{80_COH1}		CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA	
msa123961.2{80_M781}		CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA	
msa123961.2{801_JM9130013}		CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA	
msa123961.2{80_18RS21}		CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA	
msa123961.2{80h_CJB110}		CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA	
Consensus		*****	*****	*****	*****	*****	
msa123961.2{80_2603}	451	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA	500
msa123961.2{80_A909}		AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA	
msa123961.2{80_M732}		AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA	
msa123961.2{80_090}		AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA	
msa123961.2{80_COH1}		AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA	
msa123961.2{80_M781}		AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA	
msa123961.2{801_JM9130013}		AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA	

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{80_18RS21}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA
msa123961.2{80h_CJB110}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80_A909}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80_M732}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80_090}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80_COH1}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80_M781}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{801_JM9130013}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80_18RS21}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80h_CJB110}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_A909}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_M732}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_090}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_COH1}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_M781}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{801_JM9130013}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_18RS21}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80h_CJB110}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAa	AATTAGGTCA
msa123961.2{80_A909}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAa	AATTAGGTCA
msa123961.2{80_M732}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAa	AATTAGGTCA
msa123961.2{80_090}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAa	AATTAGGTCA
msa123961.2{80_COH1}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAa	AATTAGGTCA
msa123961.2{80_M781}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAa	AATTAGGTCA
msa123961.2{801_JM9130013}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAa	AATTAGGTCA
msa123961.2{80_18RS21}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAa	AATTAGGTCA
msa123961.2{80h_CJB110}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAa	AATTAGGTCA
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80_A909}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80_M732}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80_090}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80_COH1}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80_M781}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{801_JM9130013}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80_18RS21}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80h_CJB110}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_A909}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_M732}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_090}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_COH1}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_M781}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{801_JM9130013}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_18RS21}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80h_CJB110}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_A909}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_M732}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_090}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_COH1}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_M781}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{801_JM9130013}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_18RS21}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80h_CJB110}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACATTGAT	GAACCAACAG
msa123961.2{80_A909}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACATTGAT	GAACCAACAG
msa123961.2{80_M732}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACATTGAT	GAACCAACAG
msa123961.2{80_090}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACATTGAT	GAACCAACAG
msa123961.2{80_COH1}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACATTGAT	GAACCAACAG
msa123961.2{80_M781}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACATTGAT	GAACCAACAG

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{801_JM9130013}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_18RS21}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80h_CJB110}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
Consensus	*****	*****	*****	*****	*****
	851				900
msa123961.2{80_2603}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_A909}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_M732}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_090}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_COH1}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_M781}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{801_JM9130013}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_18RS21}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80h_CJB110}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
Consensus	*****	*****	*****	*****	*****
	901				950
msa123961.2{80_2603}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
msa123961.2{80_A909}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
msa123961.2{80_M732}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
msa123961.2{80_090}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
msa123961.2{80_COH1}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
msa123961.2{80_M781}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
msa123961.2{801_JM9130013}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
msa123961.2{80_18RS21}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
msa123961.2{80h_CJB110}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
Consensus	*****	*****	*****	*****	*****
	951				1000
msa123961.2{80_2603}	TCCTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80_A909}	TCCTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80_M732}	TCCTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80_090}	TCCTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80_COH1}	TCCTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80_M781}	TCCTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{801_JM9130013}	TCCTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80_18RS21}	TCCTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80h_CJB110}	TCCTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
Consensus	*****	*****	*****	*****	*****
	1001				1050
msa123961.2{80_2603}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
msa123961.2{80_A909}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
msa123961.2{80_M732}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
msa123961.2{80_090}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
msa123961.2{80_COH1}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
msa123961.2{80_M781}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
msa123961.2{801_JM9130013}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
msa123961.2{80_18RS21}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
msa123961.2{80h_CJB110}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
Consensus	*****	*****	*****	*****	*****
	1051				1100
msa123961.2{80_2603}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80_A909}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80_M732}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80_090}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80_COH1}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80_M781}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{801_JM9130013}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80_18RS21}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80h_CJB110}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
Consensus	*****	*****	*****	*****	*****
	1101				1150
msa123961.2{80_2603}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_A909}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_M732}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_090}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_COH1}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_M781}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{801_JM9130013}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_18RS21}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80h_CJB110}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
Consensus	*****	*****	*****	*****	*****
	1151				1200
msa123961.2{80_2603}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG
msa123961.2{80_A909}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG
msa123961.2{80_M732}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG
msa123961.2{80_090}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG
msa123961.2{80_COH1}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{80_M781}	GATTGTGAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCCTGAG
msa123961.2{801_JM9130013}	GATTGTGAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCCTGAG
msa123961.2{80_18RS21}	GATTGTGAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCCTGAG
msa123961.2{80h_CJB110}	GATTGTGAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCCTGAG
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80_A909}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80_M732}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80_090}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80_COH1}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80_M781}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{801_JM9130013}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80_18RS21}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80h_CJB110}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_A909}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_M732}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_090}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_COH1}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_M781}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{801_JM9130013}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_18RS21}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80h_CJB110}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_A909}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_M732}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_090}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_COH1}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_M781}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{801_JM9130013}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_18RS21}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80h_CJB110}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80_A909}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80_M732}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80_090}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80_COH1}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80_M781}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{801_JM9130013}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80_18RS21}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80h_CJB110}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	CAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_A909}	CAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_M732}	CAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_090}	CAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_COH1}	CAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_M781}	CAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{801_JM9130013}	CAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_18RS21}	CAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80h_CJB110}	CAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80_A909}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80_M732}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80_090}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80_COH1}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80_M781}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{801_JM9130013}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80_18RS21}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80h_CJB110}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80_A909}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80_M732}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80_090}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{80_COH1}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80_M781}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{801_JM9130013}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80_18RS21}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80h_CJB110}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	acgtccttca	atccctaata	ctgggtggtat	tggtacggct	atctttgtcg
msa123961.2{80_A909}	acgtccttca	-----	-----	-----	-----
msa123961.2{80_M732}	acgtccttca	-----	-----	-----	-----
msa123961.2{80_090}	acgtccttca	-----	-----	-----	-----
msa123961.2{80_COH1}	acgtccttca	-----	-----	-----	-----
msa123961.2{80_M781}	acgtccttca	-----	-----	-----	-----
msa123961.2{801_JM9130013}	acgtccttca	-----	-----	-----	-----
msa123961.2{80_18RS21}	acgtccttca	-----	-----	-----	-----
msa123961.2{80h_CJB110}	acgtccttca	-----	-----	-----	-----
Consensus	-----	-----	-----	-----	-----
msa123961.2{80_2603}	ctatcggtgc	tgccggtgatg	gcttttgcgtg	ttaaggggat	gaagcgtcgt
msa123961.2{80_A909}	-----	-----	-----	-----	-----
msa123961.2{80_M732}	-----	-----	-----	-----	-----
msa123961.2{80_090}	-----	-----	-----	-----	-----
msa123961.2{80_COH1}	-----	-----	-----	-----	-----
msa123961.2{80_M781}	-----	-----	-----	-----	-----
msa123961.2{801_JM9130013}	-----	-----	-----	-----	-----
msa123961.2{80_18RS21}	-----	-----	-----	-----	-----
msa123961.2{80h_CJB110}	-----	-----	-----	-----	-----
Consensus	-----	-----	-----	-----	-----
msa123961.2{80_2603}	acaaaagata	ac			
msa123961.2{80_A909}	-----	--			
msa123961.2{80_M732}	-----	--			
msa123961.2{80_090}	-----	--			
msa123961.2{80_COH1}	-----	--			
msa123961.2{80_M781}	-----	--			
msa123961.2{801_JM9130013}	-----	--			
msa123961.2{80_18RS21}	-----	--			
msa123961.2{80h_CJB110}	-----	--			
Consensus	-----	--			

SEQ ID NO. 8710
STRAIN 2603 frame: 1
MKLSKKLFLSAAVLTVMAGSTVEPVAQFATGMSIVRAAEVSQERPAKTTVNIYKLQADSY
KSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFKRYKVKTDISVDELKKLTVEAAD
AKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLYVEDLKNSPSNITKAYAVPFVLEL
PVANSTGTGFLSEINIYPKNVVTDEPKTDKDKVKKLGQDDAGYTI GEEFKWFLKSTIPANL
GDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHYTIDEPTVDNONTLKITFKPEKFK
EIAELLKGMTLVKNQDALDKATANTDDAAFLAIPVASTINEKAVLGKAIENTFELQYDHT
PDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLGGAFFDLLASDGTAVKWTDALIKA
NTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVDANAEGTAVTYKLKETKAPEGYVI
PDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNKRPSIPTGIGITAI FVAIGAAMV
AFAVKGMKRRTKDN

SEQ ID NO. 8711
STRAIN 090 frame: 1
AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKKLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
VEDLKNSPSNITKAYAVPFVLEL PVANSTGTGFLSEINIYPKNVVTDEPKTDKDKVKKLGQ
DDAGYTI GEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNONTLKITFKPEKFK EIAELLKGMTLVKNQDALDKATANTDDAAFLAIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
GAFFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8712
STRAIN 18RS21 frame: 1
AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKKLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
VEDLKNSPSNITKAYAVPFVLEL PVANSTGTGFLSEINIYPKNVVTDEPKTDKDKVKKLGQ
DDAGYTI GEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNONTLKITFKPEKFK EIAELLKGMTLVKNQDALDKATANTDDAAFLAIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
GAFFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8713
STRAIN M732 frame: 1
AEVSQERPAKTTVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK

Table 87: Comparative Sequences relating to SAG0645

RYKVKTDISVDELKLLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIIEEFKWLKSTIPANLGDYKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKIIFKPEKFKIEAELLKGMTLVKNQDALDKATANTDDAAFLIEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLSHTDGTFEIKGLAYAVD
ANABGTAVTYKLETKAPEGYVIPDKEIEFTVSQTSYNTKPTDIITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8714

STRAIN M781 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVINSYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKLLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIIEEFKWLKSTIPANLGDYKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKIIFKPEKFKIEAELLKGMTLVKNQDALDKATANTDDAAFLIEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLSHTDGTFEIKGLAYAVD
ANABGTAVTYKLETKAPEGYVIPDKEIEFTVSQTSYNTKPTDIITVDSADATPDTIKNNK
R

SEQ ID NO. 8715

STRAIN COH1 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVINSYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKLLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIIEEFKWLKSTIPANLGDYKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKIIFKPEKFKIEAELLKGMTLVKNQDALDKATANTDDAAFLIEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLSHTDGTFEIKGLAYAVD
ANABGTAVTYKLETKAPEGYVIPDKEIEFTVSQTSYNTKPTDIITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8716

STRAIN CJB110 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVINSYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKLLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIIEEFKWLKSTIPANLGDYKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKIIFKPEKFKIEAELLKGMTLVKNQDALDKATANTDDAAFLIEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLSHTDGTFEIKGLAYAVD
ANABGTAVTYKLETKAPEGYVIPDKEIEFTVSQTSYNTKPTDIITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8717

STRAIN JM9130013 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVINSYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKLLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIIEEFKWLKSTIPANLGDYKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKIIFKPEKFKIEAELLKGMTLVKNQDALDKATANTDDAAFLIEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLSHTDGTFEIKGLAYAVD
ANABGTAVTYKLETKAPEGYVIPDKEIEFTVSQTSYNTKPTDIITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8718

STRAIN A909 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVINSYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKLLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIIEEFKWLKSTIPANLGDYKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKIIFKPEKFKIEAELLKGMTLVKNQDALDKATANTDDAAFLIEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLSHTDGTFEIKGLAYAVD
ANABGTAVTYKLETKAPEGYVIPDKEIEFTVSQTSYNTKPTDIITVDSADATPDTIKNNK

PRETTY of: /biotmp/msa124060.2{*} April 30, 2003 07:19 ..

	1		50
msa124060.2{80_2603}	mklskklifs aavltmvags tvepvafat gmsivraAEV	SQERPAKTTv	
msa124060.2{80_M732}	-----	-----AEV	SQERPAKTTv
msa124060.2{80_A909}	-----	-----AEV	SQERPAKTTv
msa124060.2{80_090}	-----	-----AEV	SQERPAKTTv
msa124060.2{80_M781}	-----	-----AEV	SQERPAKTTv
msa124060.2{80_COH1}	-----	-----AEV	SQERPAKTTv
msa124060.2{801_JM9130013}	-----	-----AEV	SQERPAKTTv
msa124060.2{80_18RS21}	-----	-----AEV	SQERPAKTTv
msa124060.2{80h_CJB110}	-----	-----AEV	SQERPAKTTv
Consensus	-----	-----***	*****

Table 87: Comparative Sequences relating to SAG0645

	51		100
msa124060.2{80_2603}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
msa124060.2{80_M732}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
msa124060.2{80_A909}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
msa124060.2{80_090}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
msa124060.2{80_M781}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
msa124060.2{80_COH1}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
msa124060.2{801_JM9130013}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
msa124060.2{80_18RS21}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
msa124060.2{80h_CJB110}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
Consensus	***** **_**_****	*****	*****
	101		150
msa124060.2{80_2603}	VKTDISVDEL/ KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
msa124060.2{80_M732}	VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
msa124060.2{80_A909}	VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
msa124060.2{80_090}	VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
msa124060.2{80_M781}	VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
msa124060.2{80_COH1}	VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
msa124060.2{801_JM9130013}	VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
msa124060.2{80_18RS21}	VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
msa124060.2{80h_CJB110}	VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
Consensus	*****	*****	*****
	151		200
msa124060.2{80_2603}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
msa124060.2{80_M732}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
msa124060.2{80_A909}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
msa124060.2{80_090}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
msa124060.2{80_M781}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
msa124060.2{80_COH1}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
msa124060.2{801_JM9130013}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
msa124060.2{80_18RS21}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
msa124060.2{80h_CJB110}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
Consensus	*****	*****	*****
	201		250
msa124060.2{80_2603}	VVTDEPKTDK DVKkLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
msa124060.2{80_M732}	VVTDEPKTDK DVKkLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
msa124060.2{80_A909}	VVTDEPKTDK DVKkLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
msa124060.2{80_090}	VVTDEPKTDK DVKkLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
msa124060.2{80_M781}	VVTDEPKTDK DVKkLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
msa124060.2{80_COH1}	VVTDEPKTDK DVKkLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
msa124060.2{801_JM9130013}	VVTDEPKTDK DVKkLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
msa124060.2{80_18RS21}	VVTDEPKTDK DVKkLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
msa124060.2{80h_CJB110}	VVTDEPKTDK DVKkLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
Consensus	***** **_**_****	*****	*****
	251		300
msa124060.2{80_2603}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
msa124060.2{80_M732}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
msa124060.2{80_A909}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
msa124060.2{80_090}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
msa124060.2{80_M781}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
msa124060.2{80_COH1}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
msa124060.2{801_JM9130013}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
msa124060.2{80_18RS21}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
msa124060.2{80h_CJB110}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
Consensus	*****	*****	*****
	301		350
msa124060.2{80_2603}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
msa124060.2{80_M732}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
msa124060.2{80_A909}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
msa124060.2{80_090}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
msa124060.2{80_M781}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
msa124060.2{80_COH1}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
msa124060.2{801_JM9130013}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
msa124060.2{80_18RS21}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
msa124060.2{80h_CJB110}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
Consensus	*****	*****	*****
	351		400
msa124060.2{80_2603}	NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE		
msa124060.2{80_M732}	NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE		
msa124060.2{80_A909}	NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE		
msa124060.2{80_090}	NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE		
msa124060.2{80_M781}	NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE		
msa124060.2{80_COH1}	NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE		
msa124060.2{801_JM9130013}	NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE		
msa124060.2{80_18RS21}	NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE		
msa124060.2{80h_CJB110}	NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE		
Consensus	*****	*****	*****

Table 87: Comparative Sequences relating to SAG0645

	401			450
msa124060.2{80_2603}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
msa124060.2{80_M732}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
msa124060.2{80_A909}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
msa124060.2{80_090}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
msa124060.2{80_M781}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
msa124060.2{80_COH1}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
msa124060.2{801_JM9130013}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
msa124060.2{80_18RS21}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
msa124060.2{80h_CJB110}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
Consensus	*****	*****	*****	*****
	451			500
msa124060.2{80_2603}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNtKPTD
msa124060.2{80_M732}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNtKPTD
msa124060.2{80_A909}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNtKPTD
msa124060.2{80_090}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNtKPTD
msa124060.2{80_M781}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNtKPTD
msa124060.2{80_COH1}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNtKPTD
msa124060.2{801_JM9130013}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNtKPTD
msa124060.2{80_18RS21}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNtKPTD
msa124060.2{80h_CJB110}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNpKPTD
Consensus	*****	*****	*****	*****
	501			550
msa124060.2{80_2603}	ITVDSADATP	DTIKNNkrps	ipntggigta	ifvaigaavm afavkgmkrr
msa124060.2{80_M732}	ITVDSADATP	DTIKNNkrps	-----	-----
msa124060.2{80_A909}	ITVDSADATP	DTIKNN----	-----	-----
msa124060.2{80_090}	ITVDSADATP	DTIKNNkrps	-----	-----
msa124060.2{80_M781}	ITVDSADATP	DTIKNNkr--	-----	-----
msa124060.2{80_COH1}	ITVDSADATP	DTIKNNkrps	-----	-----
msa124060.2{801_JM9130013}	ITVDSADATP	DTIKNNkrps	-----	-----
msa124060.2{80_18RS21}	ITVDSADATP	DTIKNNkrps	-----	-----
msa124060.2{80h_CJB110}	ITVDSADATP	DTIKNNkrps	-----	-----
Consensus	*****	*****	-----	-----
	551			
msa124060.2{80_2603}	tkdn			
msa124060.2{80_M732}	----			
msa124060.2{80_A909}	----			
msa124060.2{80_090}	----			
msa124060.2{80_M781}	----			
msa124060.2{80_COH1}	----			
msa124060.2{801_JM9130013}	----			
msa124060.2{80_18RS21}	----			
msa124060.2{80h_CJB110}	----			
Consensus	----			

Table 88: Comparative Sequences relating to SAG0477

SEQ ID NO. 8801

STRAIN 2603

ATGCCCTAAGAAGAAATCAGATACCCAGAAAAAGAAGATTGTCTTAACGGAATGGCAA
 AAGCGTAACCTTGAATTTTAAAAAACGCAAGAGATGAAGAAGAACAAAAACGTATT
 AACGAAAAATTACGCTTAGATAAAAAGAGTAAATTAATATTCTCTCCTGAAGAACCT
 CAAATACCTACTAAAATTAAGAAGCTTCATTTTCCAAAGATTCAAGACCTAAGATTGAA
 AAGAAACAGAAAAAGAAAAAATAGTCAACAGCTTAGCCAAACTAATCGCATTAGAACT
 GCACCTATATTTGTAGTAGCATTCCTAGTCATTTAGTTCCGTTTTCCTACTAATCCT
 TTTAGTAAGCAAAAAACAAATACAGTTAGTGGAAATCAGCATACCTGATGATATTTTG
 ATAGAGAAAAACGAAATATTCAAAAAACGATTAATTTCTTTCTTTAATTTTAAACATAAA
 GCTATTGAACAACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
 CAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATGTCATATGCACAT
 ACAAGCAAGGATATCAACCTGTCTTGGAACTGGAAAAAGGCTGATCCTGTAAATAGT
 TCAGAGCTACCAAGCACTTCTTAACAATTAACCTTGATAAGGAAGATAGATTAAAGCTA
 TTAATTAAAGATTAAAGGCTTTAGACCTGATTAAATAAGTGAGATTGAGGTGATAAGT
 TTAGCTGATTCTAAAACGACACCTGACCTCCTGCTGTAGATATGCACGATGGAAATAGT
 ATTAGAATACCAATTCTAAATTTAAAGAAAGACTTCTCTTTTACAAACAAATTAAGAAG
 AACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTTTACACAACAAATAAC
 ATTGAATCAACCCCTGTAAAGCAGAAGATACAAAAATAAATCAACTGATAAAACAAA
 ACACAAATGGTCAGGTTGCGGAAATAGTCAAGGACAAACAAATAACTCAAACTAAT
 CAACAAGGACACAGATAGCAACAGAGCAGGCACCTAACCTCAAAATGTTAAT

SEQ ID NO. 8802

STRAIN H36B

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGATT
 GTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCAA
 AGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGATA
 AAAGAAGTAAATTAATATTCTCTCTCCTGAAGAACCTCAAAATACTACT
 AAAATTAAGAAGCTTCATTTTCCAAAGATTTCAGACCTAAGATTGAAAA
 GAAACAGAAAAAGAAAAAATAGTCAACAGCTTAGCCAAACTAATCGCA
 TTAGAAGCTGACCTATATTTGTAGTAGCATTCCTAGTCATTTAGTTTCC
 GTTTTCTCTACTAATCCTTTTAGTAAGCAAAAAACAAATAACAGTTAGTGG
 AAATCAGCATACACCTGATGATATTTGTAGAGAAAAACGAATATTCAAA
 AAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAA
 CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
 ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCAT
 ATGCACATACAAAGCAAGGATATCAACCTGTCTTGGAACTGGAAAAAG
 GCTGATCCTGTAAATAGTTTCAAGCTACCAAGCACTTCTTAACAATTAA
 CCTTGATAAGGAAGATAGTATTAAAGCTATTAAATTAAGATTAAAGGCTT
 TAGACCTGATTAAATAAGTGAGATTGAGGTGATAAGTTTAGCTGATTCT
 AAAACGACACCTGACCTCCTGCTGTAGATATGCACGATGGAAATAGTAT
 TAGAATACCATTATCTAAATTTAAAGAAAGACTTCTTTTACAAACAAA
 TTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTT
 TACACAACCAACAAATACCATTTGAATCAACCCCTGTAAAGCAGAAGATAC
 AAAAAATAAATCAACTGATAAAACACAAACACAAATGGTCAGGTTGCGG
 AAAATAGTCAAGGACAAACAAATAACTCAATACTAATCAACAAGGACAA
 CAGATAGCAACAGAGCAGGCACCTAACCTCAAAATGTTAAT

SEQ ID NO. 8803

STRAIN 18RS21

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGATT
 GTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCAA
 AGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGATA
 AAAGAAGTAAATTAATATTCTCTCTCCTGAAGAACCTCAAAATACTACT
 AAAATTAAGAAGCTTCATTTTCCAAAGATTTCAGACCTAAGATTGAAAA
 GAAACAGAAAAAGAAAAAATAGTCAACAGCTTAGCCAAACTAATCGCA
 TTAGAAGCTGACCTATATTTGTAGTAGCATTCCTAGTCATTTAGTTTCC
 GTTTTCTCTACTAATCCTTTTAGTAAGCAAAAAACAAATAACAGTTAGTGG
 AAATCAGCATACACCTGATGATATTTGTAGAGAAAAACGAATATTCAAA
 AAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAA
 CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
 ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCAT
 ATGCACATACAAAGCAAGGATATCAACCTGTCTTGGAACTGGAAAAAG
 GCTGATCCTGTAAATAGTTTCAAGCTACCAAGCACTTCTTAACAATTAA
 CCTTGATAAGGAAGATAGTATTAAAGCTATTAAATTAAGATTAAAGGCTT
 TAGACCTGATTAAATAAGTGAGATTGAGGTGATAAGTTTAGCTGATTCT
 AAAACGACACCTGACCTCCTGCTGTAGATATGCACGATGGAAATAGTAT
 TAGAATACCATTATCTAAATTTAAAGAAAGACTTCTTTTACAAACAAA
 TTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTT
 TACACAACCAACAAATACCATTTGAATCAACCCCTGTAAAGCAGAAGATAC
 AAAAAATAAATCAACTGATAAAACACAAACACAAATGGTCAGGTTGCGG
 AAAATAGTCAAGGACAAACAAATAACTCAATACTAATCAACAAGGACAA
 CAGATAGCAACAGAGCAGGCACCTAACCTCAAAATGTTAAT

SEQ ID NO. 8804

STRAIN M732

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAG
 TTGTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCG
 AAAGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGA
 TAAAGAAGTAAATTAATATTCTCTCTCCTGAAGAACCTCAAAATACTA
 CTAAAAATTAAGAAGCTTCATTTTCCAAAGATTTCAAACCTAAGATTGAA
 AAGAAACAGAAAAAGAAAAAATAGTCAACAGCTTAGCCAAACTAATCG
 CATTAGAAGCTGACCTATATTGTAGTAGCATTCCTAGTCATTTAGTTT

Table 88: Comparative Sequences relating to SAG0477

CCGTTTTCCTACTAAGTCTCTTTTAGTAAGCAAAAAACAATAACAGTTAGT
 GGAAATCAGCATACACCTGATGATATTTTGATAGAAAAACGAATATTCA
 AAAAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAAC
 AACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
 CAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGC
 ATATGCACATACAAAGCAAGGATATCAGCCTGTCTTGGAACTGGAAAAA
 AGGCTGATCCTGTAAATAGTTTCAGAGCTACCAAAGCACTTCTTAACAATT
 AACCTTGATAAGGAAGATAGTATTAGCTATTAAATTAAGATTAAAGGC
 TTTAGACCTGATTAAATAAGTGAGATTCAAGGTGATAAGTTTAGCTGATT
 CTAAAAACGACACCTGACCTCCTGCTGTAGATATGCATGATGGAATAGT
 ATTAGAATACCATTTATCTAAATTTAAAGAAAGACTTCTCTTTTACAAACA
 AATTAAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAG
 TTTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGAT
 ACAAATAAATAAATACTGATAAAACACAACACAAAATGGTCAGGTTGC
 GGAAATAGTCAAGGACAAACAATAAATCAATACTAATACTAATAAGGAC
 AACAGATAGCAACAGAGCAGGCACCCACCTCAAAATGTTAAT

SEQ ID NO. 8805

STRAIN COH1

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAGTT
 GTCTTAACCGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCAA
 AGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGATA
 AAAGAAGTAAATTAATATTTCTTCTCCTGAAGAACCTCAAAATACTACT
 AAAATTAAGAAGCTTCAATTTCCAAAGATTTCAAAACCTAAGATTGAAAA
 GAAACAGAAAAAGAAAAATAGTCAACAGCTTAGCCAAAACATAATCGCA
 TTAGAACTGCACCTATATTTGTAGTAGCATTCTAGTCATTTTAGTTTCC
 GTTTTCTCTACTAAGTCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGG
 AAATCAGCATACACCTGATGATATTTTGATAGAAAAACGAATATTCAAA
 AAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAA
 CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
 ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCAT
 ATGCACATACAAAGCAAGGATATCAGCCTGTCTTGGAACTGGAAAAAAG
 GCTGATCCTGTAAATAGTTTCAGAGCTACCAAAGCACTTCTTAACAATTAA
 CCTTGATAAGGAAGATAGTATTAGCTATTAAATTAAGATTAAAGGCTT
 TAGACCTGATTAAATAAGTGAGATTCAAGGTGATAAGTTTAGCTGATTCT
 AAAACGACACCTGACCTCCTGCTGTAGATATGCATGATGGAATAGTAT
 TAGAATACCATTATCTAAATTTAAAGAAAGACTTCTTTTACAAACAAA
 TTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTT
 TACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGATAC
 AAAAAATAAATAAATACTGATAAAACACAACACAAAATGGTCAGGTTGCGG
 AAAATAGTCAAGGACAAACAATAAATCAATACTAATACTAATAAGGACAA
 CAGATAGCAACAGAGCAGGCACCCACCTCAAAATGTTAAT

SEQ ID NO. 8806

STRAIN M781

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAG
 TTGTCTTAACCGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCG
 AAAGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGA
 TAAAGAAGTAAATTAATATTTCTTCTCCTGAAGAACCTCAAAATACTA
 CTAAATTAAGAAGCTTCAATTTCCAAAGATTTCAAAACCTAAGATTGAA
 AAGAAACAGAAAAAGAAAAATAGTCAACAGCTTAGCCAAAACATAATCG
 CATTAGAAGTGCACCTATATTTGTAGTAGCATTCTAGTCATTTTAGTTT
 CCGTTTTCCTACTAAGTCTTTTAGTAAGCAAAAAACAATAACAGTTAGT
 GGAAATCAGCATACACCTGATGATATTTTGATAGAAAAACGAATATTCA
 AAAAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAAC
 AACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
 CAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGC
 ATATGCACATACAAAGCAAGGATATCAGCCTGTCTTGGAACTGGAAAAA
 AGGCTGATCCTGTAAATAGTTTCAGAGCTACCAAAGCACTTCTTAACAATT
 AACCTTGATAAGGAAGATAGTATTAGCTATTAAATTAAGATTAAAGGC
 TTTAGACCTGATTAAATAAGTGAGATTCAAGGTGATAAGTTTAGCTGATT
 CTAAAAACGACACCTGACCTCCTGCTGTAGATATGCATGATGGAATAGT
 ATTAGAATACCATTTATCTAAATTTAAAGAAAGACTTCTTTTACAAACA
 AATTAAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAG
 TTTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGAT
 ACAAATAAATAAATACTGATAAAACACAACACAAAATGGTCAGGTTGC
 GGAAATAGTCAAGGACAAACAATAAATCAATACTAATACTAATAAGGAC
 AACAGATAGCAACAGAGCAGGCACCCACCTCAAAATGTTAAT

SEQ ID NO. 8807

STRAIN CJB110

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAG
 TTGTCTTAACCGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCG
 AAAGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGA
 TAAAGAAGTAAATTAATATTTCTTCTCCTGAAGAACCTCAAAATACTA
 CTAAATTAAGAAGCTTCAATTTCCAAAGATTTCAAAACCTAAGATTGAA
 AAGAAACAGAAAAAGAAAAATAGTCAACAGCTTAGCCAAAACATAATCG
 CATTAGAAGTGCACCTATATTTGTAGTAGCATTCTAGTCATTTTAGTTT
 CCGTTTTCCTACTAAGTCTTTTAGTAAGCAAAAAACAATAACAGTTAGT
 GGAAATCAGCATACACCTGATGATATTTTGATAGAAAAACGAATATTCA
 AAAAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAAC
 AACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
 CAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGC

Table 88: Comparative Sequences relating to SAG0477

ATATGCACATACAAAGCAAGGATATCAGCCTGTCTTGGAACTGGAAAAA
 AGGCTGATCCTGTAAATAGTTCAGAGCTACCAAGCACTTCTTAACAATT
 AACCTTGATAAGGAAGATAGTATTAAAGCTATTAAATTAAGATTAAAGGC
 TTTAGACCTGATTAAATAAGTGAGATTGAGTGATAAGTTTAGCTGATT
 CTAACACGACACCTGACCTCCTGCTGTTAGATATGCATGATGGAAATAGT
 ATTAGAATACCATTATCTAAATTTAAAGAAAGACTTCTTTTACAAACA
 AATTAAAGAAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAG
 TTTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGAT
 ACAAATAATCAACTGATATAAACACAACACAATAATGGTCAGGTTGC
 GAAAAATAGTCAAGGACAAACAATAACTCAATACTAATCAACAAGGAC
 AACAGATAGCAACAGAGCAGGCACCCCAACCTCAAAATGTTAAT

SEQ ID NO. 8808

STRAIN 1169NT

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAAGT
 TGTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCA
 AAGAAGATGAAGAAGAACAAAAACGTATTAAACGAAAAATTACGCTTAGAT
 AAAAGAAGTAAATTAATATTCTTCTCCTGAAGAACCTCAAAATACTAC
 TAAATTAAGAAGCTTCATTTTCCAAAGATTCAAAACCTAAGATTGAAA
 AGAAACAGAAAAAAGAAAAATAGTCAACAGCTTAGCCAAAACCTAATCGC
 ATTAGAAGCTGCACCTATATTTAGTAGCATTCTAGTCATTTTAGTTTC
 CGTTTTCTACTAATCTCTTTTAGTAAGCAAAAAACAATAACAGTTAGTG
 GAAATCAGCATACACCTGATGATATTTGATAGAGAAAAAGCAATATTCAA
 AAAACGATTATTCTTTCTTTAATTTTAAACATAAAGCTATTGAACA
 ACCTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATC
 AATTTCCCAACAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCA
 TATGCACATACAAAGCAAGGATATCAGCCTGTCTTGGAACTGGAAAAA
 GGCTGATCCTGTAAATAGTTCAGAGCTACCAAGCACTTCTTAACAATTA
 ACCTTGATAAGGAAGATAGTATTAAAGCTATTAAATAAGATTAAAGGCT
 TTAGACCTGATTAAATAAGTGAGATTGAGGTGATAAGTTTAGCTGATT
 TAAAAAGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGTA
 TTAGAATACCATTTATCTAAATTTAAAGAAAGACTTCTTTTACAAACAA
 ATTAAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGT
 TTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGATA
 CAAAAATAAATCAACTGATATAAACACAACCCCAAAATGGTCAGGTTGCG
 GAAAAATAGTCAAGGACAAACAATACTCAATACTAATCAACAAGGACA
 ACAACAGATAGCAACGAGCAGGCACCCCAACCTCAAAATGTTAAT

SEQ ID NO. 8809

STRAIN JM9130013

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAAGT
 GTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCA
 AGAAGATGAAGAAGAACAAAAACGTATTAAACGAAAAATTACGCTTAGATA
 AAAAGAAGTAAATTAATATTCTTCTCCTGAAGAACCTCAAAATACTACT
 AAAATTAAGAAGCTTCATTTTCCAAAGATTCAAGACCTAAGATTGAAAA
 GAAACAGAAAAAAGAAAAATAGTCAACAGCTTAGCCAAAACCTAATCGCA
 TTAGAAGCTGCACCTATATTGTTAGTAGCATTCTAGTCATTTTAGTTTCC
 GTTTTCTACTAATCTCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGG
 AATCAGCATACACCTGATGATATTTGATAGAGAAAAAGCAATATTCAA
 AAAACGATTATTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAA
 CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
 ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCAT
 ATGCACATACAAAGCAAGGATATCAACCTGTCTTGGAACTGGAAAAAAG
 CCTGATCCTGTAAATAGTTCAGAGCTACCAAGCACTTCTTAACAATTA
 CCTTGATAAGGAAGATAGTATTAAAGCTATTAAATAAGATTAAAGGCTT
 TAGACCTGATTAAATAAGTGAGATTGAGGTGATAAGTTTAGCTGATTCT
 AAAACGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGTAT
 TAGAATACCATTTATCTAAATTTAAAGAAAGACTTCTTTTACAAACAAA
 TTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGT
 TACACAACAACAATAACCTTGAATCAACCCCTGTGTAAGCAGAAGATAC
 AAAAAATAAATCAACTGATATAAACACAACCAAAATGGTCAGGTTGCGG
 AAAATAGTCAAGGACAAACAATACTCAATACTAATCAACAAGGACAA
 CAGATAGCAACAGAGCAGGCACCTAACCTCAAAATGTTAAT

SEQ ID NO. 8810

STRAIN A909

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAAGTGTCT
 TTAACGGAATGGCAAAAGCGTAACCTTGAATTTTaaAAAAACGCAAGA
 AGATGAAGAAGAAaCAAAAAACGTATTAAACGAAAAATTACGCTTAGATAAAA
 GAAGTAAATTAATATTCTTCTCCTGAAGAACCTCAAAATACTACTAA
 ATTAAGAAGCTTCATTTTCCAAAGATTCAAGACCTAAGATTGAAAAGAA
 ACAGAAAAAAGAAAAATAGTCAACAGCTTAGCCAAAACCTAATCGCATTA
 GAAGTGCACCTATATTGTTAGTAGCATTCTAGTCATTTTAGTTTCCGTT
 TTCTCTAATCTCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGGAAA
 TCAGCATACACCTGATGATATTTGATAGAGAAAAAGCAATATTCAAAAA
 ACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAACGT
 TTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCAATT
 TCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCATATG
 CACATACAAAGCAAGGATATCAACCTGTCTTGGAACTGGAAAAAAGGCT
 GATCCTGTAAATAGTTCAGAGCTACCAAGCACTTCTTAACAATTAACCT
 TGATAAGGAAGATAGTATTAAAGCTATTAAATAAGATTAAAGGCTTTAG
 ACCTGATTAAATAAGTGAGATTGAGGTGATAAGTTTAGCTGATTCTAAA
 ACGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGTATTAA

Table 88: Comparative Sequences relating to SAG0477

AATACCATTATCTAAATTTAAAGAAAGACTTCCTTTTACAAACAAATTA
 AGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTTTAC
 ACAACAACAAATACCATTGAATCAACCCCTGTTAAAGCAGAAGATACAAA
 AAATAAATCAACTGATAAAACAAACCAAAATGGTCAGGTTGCGGAAA
 ATAGTCAAGGACAAACAAATAACTCAATACTAATCAACAAGGACAACAG
 ATAGCAACAGAGCAGGCACCTAACCTCAAATGTTAAT

SEQ ID NO. 8811

STRAIN 090

TAAGAAGAAATCAGATACCCAGAAAAAGAAGTTGTCTTAACGGAAT
 GGCAAAAGCGTAACCTTGAATTTTAAAAAACGCAAGAAGATGAAGAA
 GAACAAAAACGTATTAAACGAAAAATTACGCTTAGATAAAAGAAGTaaATT
 AAATATTCTCTCTCTGAAGAACCTCAAAATACTACTAAAATTAGAAGC
 TTCATTTTCCAAAGATTTCAAACCTAAGATTGAAAAGAAACGAAAAAA
 GAAAAATAGTCAACAGCTTAGCCAAAATTAATCGCATTAGAAGTGCACC
 TATATTGTTAGTAGCATTCTTAGTCAATTTAGTTTCCGTTTCTCTACTAA
 CTCTTTTAGTAAGCAAAAAACATAACAGTTAGTGGAAATCAGCATACA
 CCTGATGATATTTTATAGAAAAAACGAATATTCAAAAAACGATTATTT
 CTTTCTTTAATTTTAAACATAAAGCTATTGAACAACGTTTAGCTGCAG
 AAGATGTATGGGTAACAGCTCAGATGACTTATCAATTTCCCAATAAG
 TTTCAATTTCAAGTTCAAGAAAAATAAGATTATTGCATATGCACATACAAA
 GCAAGGATATCAGCCTGTCTTGGAACTGGAAGAAAGGCTGATCCTGTAA
 ATAGTTTCAGAGCTACCAAGCACTTCTTAACAATTAACCTTGATAAGGAA
 GATAGTATTAAAGCTATTAAATTAAGATTAAAGGCTTAGACCTGATTT
 AATAAGTGAGATTCAAGGTGATAAGTTTAGCTGATTTAAAACGACACCTG
 ACCTCCTGCTGTTAGATATGCATGATGGAATAGTATTAGAATACCATTA
 TCTAAATTTAAAGAAAGACTTCTCTTTTACAAACAAATTAAGAAGAACTT
 TAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTTTACACAACAACAA
 GTACTATTGAATCAACCCCTGTGAAAGCGGAAGATACAAAAATAAATCA
 ACTGATATAAACACAAACAAATGGTCAGGTTGCGGAAATAGTCAAGG
 ACAACAAATAACTCAATACTAATCAACAAGGACAACAGATGCAACAG
 AGCAGGCACCAACCTCAAATGTTAAT

PRETTY of: /biotmp/msa24691.2{*} August 5, 2002 05:14 ..

	1	50
msa252409.2{85_090.con}	~TAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_CJB110}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_COH1}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_M732}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_M781}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_18RS21}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_2603}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_A909}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_H36B}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_JM9130013}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_1169NT}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
Consensus	*****	*****
	51	100
msa252409.2{85_090.con}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_CJB110}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_COH1}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_M732}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_M781}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_18RS21}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_2603}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_A909}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_H36B}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_JM9130013}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_1169NT}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
Consensus	*****	*****
	101	150
msa252409.2{85_090.con}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_CJB110}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_COH1}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_M732}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_M781}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_18RS21}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_2603}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_A909}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_H36B}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_JM9130013}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_1169NT}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
Consensus	*****	*****
	151	200
msa252409.2{85_090.con}	TTAAATATTT CTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA	
msa252409.2{85_CJB110}	TTAAATATTT CTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA	
msa252409.2{85_COH1}	TTAAATATTT CTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA	
msa252409.2{85_M732}	TTAAATATTT CTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA	

Table 88: Comparative Sequences relating to SAG0477

msa252409.2{85_M781}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_18RS21}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_2603}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_A909}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_H36B}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_JM9130013}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_1169NT}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
Consensus	*****	*****	*****	*****	*****
201					
msa252409.2{85_090.con}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_CJB110}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_COH1}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_M732}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_M781}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_18RS21}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_2603}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_A909}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_H36B}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_JM9130013}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_1169NT}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
Consensus	*****	*****	***-*****	*****	*****
251					
msa252409.2{85_090.con}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_CJB110}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_COH1}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_M732}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_M781}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_18RS21}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_2603}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_A909}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_H36B}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_JM9130013}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_1169NT}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
Consensus	*****	*****	*****	*****	*****
301					
msa252409.2{85_090.con}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_CJB110}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_COH1}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_M732}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_M781}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_18RS21}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_2603}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_A909}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_H36B}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_JM9130013}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_1169NT}	CCTATATTTa	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
Consensus	*****	*****	*****	*****	*****
351					
msa252409.2{85_090.con}	AACCTCCTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_CJB110}	AACCTCCTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_COH1}	AACCTCCTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_M732}	AACCTCCTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_M781}	AACCTCCTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_18RS21}	AACCTCCTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_2603}	AACCTCCTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_A909}	AACCTCCTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_H36B}	AACCTCCTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_JM9130013}	AACCTCCTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_1169NT}	AACCTCCTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
Consensus	*****	*****	*****	*****	*****
401					
msa252409.2{85_090.con}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_CJB110}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_COH1}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_M732}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_M781}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_18RS21}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_2603}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_A909}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_H36B}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_JM9130013}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_1169NT}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
Consensus	*****	*****	***-*****	*****	*****
451					
msa252409.2{85_090.con}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
msa252409.2{85_CJB110}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
msa252409.2{85_COH1}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC

Table 88: Comparative Sequences relating to SAG0477

msa252409.2{85_M732}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC		
msa252409.2{85_M781}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC		
msa252409.2{85_18RS21}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC		
msa252409.2{85_2603}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC		
msa252409.2{85_A909}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC		
msa252409.2{85_H36B}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC		
msa252409.2{85_JM9130013}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC		
msa252409.2{85_1169NT}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC		
Consensus	*****	*****	*****	*****	*****		
msa252409.2{85_090.con}	501	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa	550
msa252409.2{85_CJB110}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa	TTTCCCAATa	
msa252409.2{85_COH1}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa	TTTCCCAATa	
msa252409.2{85_M732}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa	TTTCCCAATa	
msa252409.2{85_M781}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa	TTTCCCAATa	
msa252409.2{85_18RS21}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa	TTTCCCAATa	
msa252409.2{85_2603}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa	TTTCCCAATa	
msa252409.2{85_A909}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa	TTTCCCAATa	
msa252409.2{85_H36B}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa	TTTCCCAATa	
msa252409.2{85_JM9130013}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa	TTTCCCAATa	
msa252409.2{85_1169NT}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa	TTTCCCAATa	
Consensus	*****	*****	*****	*****	*****	*****_*	
msa252409.2{85_090.con}	551	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA	600
msa252409.2{85_CJB110}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA	TGCACATACA	
msa252409.2{85_COH1}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA	TGCACATACA	
msa252409.2{85_M732}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA	TGCACATACA	
msa252409.2{85_M781}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA	TGCACATACA	
msa252409.2{85_18RS21}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA	TGCACATACA	
msa252409.2{85_2603}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA	TGCACATACA	
msa252409.2{85_A909}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA	TGCACATACA	
msa252409.2{85_H36B}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA	TGCACATACA	
msa252409.2{85_JM9130013}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA	TGCACATACA	
msa252409.2{85_1169NT}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA	TGCACATACA	
Consensus	*****	*****	*****	*****	*****	*****	
msa252409.2{85_090.con}	601	AAGCAAGGAT	ATCAgCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT	650
msa252409.2{85_CJB110}	AAGCAAGGAT	ATCAgCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT	CTGATCCTGT	
msa252409.2{85_COH1}	AAGCAAGGAT	ATCAgCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT	CTGATCCTGT	
msa252409.2{85_M732}	AAGCAAGGAT	ATCAgCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT	CTGATCCTGT	
msa252409.2{85_M781}	AAGCAAGGAT	ATCAgCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT	CTGATCCTGT	
msa252409.2{85_18RS21}	AAGCAAGGAT	ATCAaCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT	CTGATCCTGT	
msa252409.2{85_2603}	AAGCAAGGAT	ATCAaCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT	CTGATCCTGT	
msa252409.2{85_A909}	AAGCAAGGAT	ATCAaCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT	CTGATCCTGT	
msa252409.2{85_H36B}	AAGCAAGGAT	ATCAaCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT	CTGATCCTGT	
msa252409.2{85_JM9130013}	AAGCAAGGAT	ATCAaCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT	CTGATCCTGT	
msa252409.2{85_1169NT}	AAGCAAGGAT	ATCAgCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT	CTGATCCTGT	
Consensus	*****	*****_*****	*****	*****	*****	*****	
msa252409.2{85_090.con}	651	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG	700
msa252409.2{85_CJB110}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG	CTTGATAAGG	
msa252409.2{85_COH1}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG	CTTGATAAGG	
msa252409.2{85_M732}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG	CTTGATAAGG	
msa252409.2{85_M781}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG	CTTGATAAGG	
msa252409.2{85_18RS21}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG	CTTGATAAGG	
msa252409.2{85_2603}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG	CTTGATAAGG	
msa252409.2{85_A909}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG	CTTGATAAGG	
msa252409.2{85_H36B}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG	CTTGATAAGG	
msa252409.2{85_JM9130013}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG	CTTGATAAGG	
msa252409.2{85_1169NT}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG	CTTGATAAGG	
Consensus	*****	*****	*****	*****	*****	*****	
msa252409.2{85_090.con}	701	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCGTGAT	750
msa252409.2{85_CJB110}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCGTGAT	AGACCCGTGAT	
msa252409.2{85_COH1}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCGTGAT	AGACCCGTGAT	
msa252409.2{85_M732}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCGTGAT	AGACCCGTGAT	
msa252409.2{85_M781}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCGTGAT	AGACCCGTGAT	
msa252409.2{85_18RS21}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCGTGAT	AGACCCGTGAT	
msa252409.2{85_2603}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCGTGAT	AGACCCGTGAT	
msa252409.2{85_A909}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCGTGAT	AGACCCGTGAT	
msa252409.2{85_H36B}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCGTGAT	AGACCCGTGAT	
msa252409.2{85_JM9130013}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCGTGAT	AGACCCGTGAT	
msa252409.2{85_1169NT}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCGTGAT	AGACCCGTGAT	
Consensus	*****	*****	*****	*****	*****	*****	
msa252409.2{85_090.con}	751	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC	800
msa252409.2{85_CJB110}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC	AAACGACACC	

Table 88: Comparative Sequences relating to SAG0477

msa252409.2{85_COH1}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_M732}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_M781}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_18RS21}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_2603}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_A909}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_H36B}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_JM9130013}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_1169NT}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_CJB110}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_COH1}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_M732}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_M781}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_18RS21}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_2603}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_A909}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_H36B}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_JM9130013}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_1169NT}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_CJB110}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_COH1}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_M732}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_M781}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_18RS21}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_2603}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_A909}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_H36B}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_JM9130013}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_1169NT}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAAC
msa252409.2{85_CJB110}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAAC
msa252409.2{85_COH1}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAAC
msa252409.2{85_M732}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAAC
msa252409.2{85_M781}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAAC
msa252409.2{85_18RS21}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAAC
msa252409.2{85_2603}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAAC
msa252409.2{85_A909}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAAC
msa252409.2{85_H36B}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAAC
msa252409.2{85_JM9130013}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAAC
msa252409.2{85_1169NT}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAAC
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT
msa252409.2{85_CJB110}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT
msa252409.2{85_COH1}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT
msa252409.2{85_M732}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT
msa252409.2{85_M781}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT
msa252409.2{85_18RS21}	AAaTACcATT	GAATCAACCC	CTGTtAAAGC	aGAAGATACA	AAAAATAAAT
msa252409.2{85_2603}	AAaTACcATT	GAATCAACCC	CTGTtAAAGC	aGAAGATACA	AAAAATAAAT
msa252409.2{85_A909}	AAaTACcATT	GAATCAACCC	CTGTtAAAGC	aGAAGATACA	AAAAATAAAT
msa252409.2{85_H36B}	AAaTACcATT	GAATCAACCC	CTGTtAAAGC	aGAAGATACA	AAAAATAAAT
msa252409.2{85_JM9130013}	AAaTACcATT	GAATCAACCC	CTGTtAAAGC	aGAAGATACA	AAAAATAAAT
msa252409.2{85_1169NT}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT
Consensus	**--***--***	*****	****--****	*****	*****
msa252409.2{85_090.con}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_CJB110}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_COH1}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_M732}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_M781}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_18RS21}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_2603}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_A909}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_H36B}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_JM9130013}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_1169NT}	CAACTGATAA	AACACAAaCc	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
Consensus	*****	*****--	*****	*****	*****
msa252409.2{85_090.con}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC

Table 88: Comparative Sequences relating to SAG0477

msa252409.2{85_CJB110}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_COH1}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_M732}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_M781}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_18RS21}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_2603}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_A909}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_H36B}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_JM9130013}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_1169NT}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGGacaAC	AACAGATAGC
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	1101				1134
msa252409.2{85_CJB110}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT	TAAT	
msa252409.2{85_COH1}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT	TAAT	
msa252409.2{85_M732}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT	TAAT	
msa252409.2{85_M781}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT	TAAT	
msa252409.2{85_18RS21}	AACaGAGCAG	GCACCtAACC	CTCAAAATGT	TAAT	
msa252409.2{85_2603}	AACaGAGCAG	GCACCtAACC	CTCAAAATGT	TAAT	
msa252409.2{85_A909}	AACaGAGCAG	GCACCtAACC	CTCAAAATGT	TAAT	
msa252409.2{85_H36B}	AACaGAGCAG	GCACCtAACC	CTCAAAATGT	TAAT	
msa252409.2{85_JM9130013}	AACaGAGCAG	GCACCtAACC	CTCAAAATGT	TAAT	
msa252409.2{85_1169NT}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT	TAAT	
Consensus	***-*****	*****-****	*****	****	

SEQ ID NO. 8812

STRAIN 2603 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEEPQ
 NTTKI KKLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTAPI FVVAFLVILVSVFLLTPF
 SKQKTIITVSGNQHTPPDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPNVNSSELPHKFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVLSLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPHYKQIKKN
 LKEPSIVDMEVGVTITNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNNSTNQ
 GQQQIATEQAPNPQNVN

SEQ ID NO. 8813

STRAIN H36B frame: 1

PKKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEEPQ
 NTTKI KKLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTAPI FVVAFLVILVSVFLLTPF
 SKQKTIITVSGNQHTPPDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPNVNSSELPHKFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVLSLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPHYKQIKKN
 LKEPSIVDMEVGVTITNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNNSTNQ
 GQQQIATEQAPNPQNVN

SEQ ID NO. 8814

STRAIN 18RS21 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEEPQ
 NTTKI KKLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTAPI FVVAFLVILVSVFLLTPF
 SKQKTIITVSGNQHTPPDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPNVNSSELPHKFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVLSLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPHYKQIKKN
 LKEPSIVDMEVGVTITNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNNSTNQ
 GQQQIATEQAPNPQNVN

SEQ ID NO. 8815

STRAIN M732 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEEPQ
 NTTKI KKLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTAPI FVVAFLVILVSVFLLTPF
 SKQKTIITVSGNQHTPPDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPNVNSSELPHKFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVLSLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPHYKQIKKN
 LKEPSIVDMEVGVTITNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNNSTNQ
 GQQQIATEQAPNPQNVN

SEQ ID NO. 8816

STRAIN COH1 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEEPQ
 NTTKI KKLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTAPI FVVAFLVILVSVFLLTPF
 SKQKTIITVSGNQHTPPDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPNVNSSELPHKFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVLSLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPHYKQIKKN
 LKEPSIVDMEVGVTITNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNNSTNQ
 GQQQIATEQAPNPQNVN

SEQ ID NO. 8817

STRAIN M781 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEEPQ

Table 88: Comparative Sequences relating to SAG0477

NTTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRI RTAPIFVVAFLVILVSVFLLTPF
 SKQKTI TVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPVNSSEL PKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKS TDKTQTQNGQVAENSQGGTNNNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8818

STRAIN CJB110 frame: 1

PKKKS DTPKEKEEVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
 NTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRI RTAPIFVVAFLVILVSVFLLTPF
 SKQKTI TVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPVNSSEL PKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKS TDKTQTQNGQVAENSQGGTNNNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8819

STRAIN 1169NT frame: 1

PKKKS DTPKEKEEVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
 NTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRI RTAPIFVVAFLVILVSVFLLTPF
 SKQKTI TVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPVNSSEL PKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKS TDKTQTQNGQVAENSQGGTNNNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8820

STRAIN JM9130013 frame: 1

PKKKS DTPKEKEEVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
 NTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRI RTAPIFVVAFLVILVSVFLLTPF
 SKQKTI TVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPVNSSEL PKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVYTTTNTIESTPVKAEDTKNKS TDKTQTQNGQVAENSQGGTNNNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8821

STRAIN A909 frame: 1

PKKKS DTPKEKEEVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
 NTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRI RTAPIFVVAFLVILVSVFLLTPF
 SKQKTI TVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPVNSSEL PKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIXIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVYTTTNTIESTPVKAEDTKNKS TDKTQTQNGQVAENSQGGTNNNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8822

STRAIN 090 frame: 2

KKKS DTPKEKEEVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
 TTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRI RTAPIFVVAFLVILVSVFLLTPF
 KQKTI TVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAEDVWVKTAQMTYQ
 PNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPVNSSEL PKHFLTINLDKEDSIKLLI
 KDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKNL
 KEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKS TDKTQTQNGQVAENSQGGTNNNTNQ
 QGQQIATEQAPNPQNVN

PRETTY of: /biotmp/msa252337.2{*} January 31, 2003 03:32 ..

	1	50
msa252337.2{85_090}	-KKKS DTPKEK	EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_18RS21}	PKKKS DTPKEK	EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_2603}	PKKKS DTPKEK	EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_A909}	PKKKS DTPKEK	EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_CJB110}	PKKKS DTPKEK	EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_COH1}	PKKKS DTPKEK	EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_H36B}	PKKKS DTPKEK	EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_JM9130013}	PKKKS DTPKEK	EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_M732}	PKKKS DTPKEK	EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_M781}	PKKKS DTPKEK	EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_1169NT}	PKKKS DTPKEK	EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
Consensus	*****	*****
	51	100
msa252337.2{85_090}	LNISSPEEPQ	NTTKIKKLHF PKISrPKIEK QKQKEKIVNS LAKTNRI RTA
msa252337.2{85_18RS21}	LNISSPEEPQ	NTTKIKKLHF PKISrPKIEK QKQKEKIVNS LAKTNRI RTA
msa252337.2{85_2603}	LNISSPEEPQ	NTTKIKKLHF PKISrPKIEK QKQKEKIVNS LAKTNRI RTA
msa252337.2{85_A909}	LNISSPEEPQ	NTTKIKKLHF PKISrPKIEK QKQKEKIVNS LAKTNRI RTA
msa252337.2{85_CJB110}	LNISSPEEPQ	NTTKIKKLHF PKISrPKIEK QKQKEKIVNS LAKTNRI RTA

Table 88: Comparative Sequences relating to SAG0477

msa252337.2{85_COH1}	LNISSPPEEPQ	NTTKIKKLHF	PKISkPKIEK	KQKKEKIVNS	LAKTNRIRTA
msa252337.2{85_H36B}	LNISSPPEEPQ	NTTKIKKLHF	PKISrPKIEK	KQKKEKIVNS	LAKTNRIRTA
msa252337.2{85_JM9130013}	LNISSPPEEPQ	NTTKIKKLHF	PKISrPKIEK	KQKKEKIVNS	LAKTNRIRTA
msa252337.2{85_M732}	LNISSPPEEPQ	NTTKIKKLHF	PKISkPKIEK	KQKKEKIVNS	LAKTNRIRTA
msa252337.2{85_M781}	LNISSPPEEPQ	NTTKIKKLHF	PKISkPKIEK	KQKKEKIVNS	LAKTNRIRTA
msa252337.2{85_1169NT}	LNISSPPEEPQ	NTTKIKKLHF	PKISkPKIEK	KQKKEKIVNS	LAKTNRIRTA
Consensus	*****	*****	****_****	*****	*****
msa252337.2{85_090}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_18RS21}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_2603}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_A909}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_CJB110}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_COH1}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_H36B}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_JM9130013}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_M732}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_M781}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_1169NT}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
Consensus	***_****	*****	*****	*****	*****
msa252337.2{85_090}	FFSLIFKHKA	IEORLAAEDV	WVKTAQMTYQ	FPNKFHIVQV	ENKI IAYAHT
msa252337.2{85_18RS21}	FFSLIFKHKA	IEORLAAEDV	WVKTAQMTYQ	FPNKFHIVQV	ENKI IAYAHT
msa252337.2{85_2603}	FFSLIFKHKA	IEORLAAEDV	WVKTAQMTYQ	FPNKFHIVQV	ENKI IAYAHT
msa252337.2{85_A909}	FFSLIFKHKA	IEORLAAEDV	WVKTAQMTYQ	FPNKFHIVQV	ENKI IAYAHT
msa252337.2{85_CJB110}	FFSLIFKHKA	IEORLAAEDV	WVKTAQMTYQ	FPNKFHIVQV	ENKI IAYAHT
msa252337.2{85_COH1}	FFSLIFKHKA	IEORLAAEDV	WVKTAQMTYQ	FPNKFHIVQV	ENKI IAYAHT
msa252337.2{85_H36B}	FFSLIFKHKA	IEORLAAEDV	WVKTAQMTYQ	FPNKFHIVQV	ENKI IAYAHT
msa252337.2{85_JM9130013}	FFSLIFKHKA	IEORLAAEDV	WVKTAQMTYQ	FPNKFHIVQV	ENKI IAYAHT
msa252337.2{85_M732}	FFSLIFKHKA	IEORLAAEDV	WVKTAQMTYQ	FPNKFHIVQV	ENKI IAYAHT
msa252337.2{85_M781}	FFSLIFKHKA	IEORLAAEDV	WVKTAQMTYQ	FPNKFHIVQV	ENKI IAYAHT
msa252337.2{85_1169NT}	FFSLIFKHKA	IEORLAAEDV	WVKTAQMTYQ	FPNKFHIVQV	ENKI IAYAHT
Consensus	*****	*****	*****	*****	*****
msa252337.2{85_090}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_18RS21}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_2603}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_A909}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_CJB110}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_COH1}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_H36B}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_JM9130013}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_M732}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_M781}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_1169NT}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
Consensus	*****	*****	*****	*****	*****
msa252337.2{85_090}	LISEIQVISL	ADSKITPDLL	LLDMHDGNSI	rIPLSKFKER	LPFFYKQIKKN
msa252337.2{85_18RS21}	LISEIQVISL	ADSKITPDLL	LLDMHDGNSI	rIPLSKFKER	LPFFYKQIKKN
msa252337.2{85_2603}	LISEIQVISL	ADSKITPDLL	LLDMHDGNSI	rIPLSKFKER	LPFFYKQIKKN
msa252337.2{85_A909}	LISEIQVISL	ADSKITPDLL	LLDMHDGNSI	xIPLSKFKER	LPFFYKQIKKN
msa252337.2{85_CJB110}	LISEIQVISL	ADSKITPDLL	LLDMHDGNSI	rIPLSKFKER	LPFFYKQIKKN
msa252337.2{85_COH1}	LISEIQVISL	ADSKITPDLL	LLDMHDGNSI	rIPLSKFKER	LPFFYKQIKKN
msa252337.2{85_H36B}	LISEIQVISL	ADSKITPDLL	LLDMHDGNSI	rIPLSKFKER	LPFFYKQIKKN
msa252337.2{85_JM9130013}	LISEIQVISL	ADSKITPDLL	LLDMHDGNSI	rIPLSKFKER	LPFFYKQIKKN
msa252337.2{85_M732}	LISEIQVISL	ADSKITPDLL	LLDMHDGNSI	rIPLSKFKER	LPFFYKQIKKN
msa252337.2{85_M781}	LISEIQVISL	ADSKITPDLL	LLDMHDGNSI	rIPLSKFKER	LPFFYKQIKKN
msa252337.2{85_1169NT}	LISEIQVISL	ADSKITPDLL	LLDMHDGNSI	rIPLSKFKER	LPFFYKQIKKN
Consensus	*****	*****	*****	-*****	*****
msa252337.2{85_090}	LKEPSIVDME	GVVYTTTtTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_18RS21}	LKEPSIVDME	GVVYTTTnTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_2603}	LKEPSIVDME	GVVYTTTnTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_A909}	LKEPSIVDME	GVVYTTTnTI	ESTPVKAEDT	KNKSTDKTQx	QNGQVAENSQ
msa252337.2{85_CJB110}	LKEPSIVDME	GVVYTTTtTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_COH1}	LKEPSIVDME	GVVYTTTtTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_H36B}	LKEPSIVDME	GVVYTTTnTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_JM9130013}	LKEPSIVDME	GVVYTTTnTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_M732}	LKEPSIVDME	GVVYTTTtTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_M781}	LKEPSIVDME	GVVYTTTtTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_1169NT}	LKEPSIVDME	GVVYTTTtTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
Consensus	*****	*****_**	*****	*****_	*****
msa252337.2{85_090}	GQTNNNSNTNQ	QGQQiatega	pnpqnv-		
msa252337.2{85_18RS21}	GQTNNNSNTNQ	QGQQiatega	pnpqnv-		
msa252337.2{85_2603}	GQTNNNSNTNQ	QGQQiatega	pnpqnv-		
msa252337.2{85_A909}	GQTNNNSNTNQ	QGQQiatega	pnpqnv-		

Table 88: Comparative Sequences relating to SAG0477

msa252337.2{85_CJB110}	GQTNNSENTNQ	QGQQiateqa	pnpqnv-
msa252337.2{85_COH1}	GQTNNSENTNQ	QGQQiateqa	pnpqnv-
msa252337.2{85_H36B}	GQTNNSENTNQ	QGQQiateqa	pnpqnv-
msa252337.2{85_JM9130013}	GQTNNSENTNQ	QGQQiateqa	pnpqnv-
msa252337.2{85_M732}	GQTNNSENTNQ	QGQQiateqa	pnpqnv-
msa252337.2{85_M781}	GQTNNSENTNQ	QGQQiateqa	pnpqnv-
msa252337.2{85_1169NT}	GQTNNSENTNQ	QGQQiateq	apnpqnv
Consensus	*****	****-	-*****

Table 89: Comparative Sequences relating to SAG1350

SEQ ID NO. 8901

STRAIN 2603

ATGAAAAAGGACAAAGTAAATGATACTAAGCAATCTTACTCTCTACGTAAA
 TATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTACATAATGGTCACAACTCCTGTT
 TTTGCGGATCAAACATACATCGGTTCAAGTTAATAATCAGACAGGCCTAGTGTGGATGCT
 AATAATTCCTCCAATGAGACAAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGT
 CAAGCGTCTGATAAAGTTGTAAGTAGTCAAAATACGGCAACAAAGGACATTACTACTCCT
 TTAGTAGAGACAAAGCCATGGTGGAAAAACATTACCTGAACAAGGGAATTATGTTTAT
 AGCAAGAAACCGAGGTGAAAAATACACCTTCAAATCAGCCCCAGTAGCTTTCTATGCA
 AAGAAAGGTGATAAAGTTTCTATGACCAAGTATTTAATAAAGATAATGTGAAATGGATT
 TCATATAAGTCTTTTGTGGCGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCA
 GGAGGTTTCAGAGACTAAAGCACCTACTCCTGTAAACAAATTCAGGAAGCAATAATCAAGAG
 AAAATAGCAACGCAAGGAAATATACATTTTCACATAAAGTAGAAGTAAAAAATGAAGCT
 AAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGAGACAGAATTTTTTACGACCAA
 ATACTAACTATTGAAGGAAATCAGTGGTTATCTTATAAATCAITCAATGGTGTTCGTCGT
 TTTGTTTGTCTAGGTAAAGCATCTTCACTAGAAAAAATGAAGATAAAGAAAAAGTGTCT
 CCTCAACCAAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACAACT
 ACAGGTTTTGATATTTTAAATTACGAATATTAAAGATGATAACGGTATCGTGTCTTAAAG
 GTACCGGTTTGGACTGAACAAGGAGGCAAGATGATATTAAATGGGTATACAGCTGTAAT
 ACTGGGGATGGCACTACAAAGTAGCTGTATCATTTGCTGACCATAAAGATGAGAAGGGT
 CTTTATAATATTCTTTTACTACCAAGAGCTAGTGGGACACTTGTAGGTGTAAACAGGA
 ACTAAAGTGACAGTAGCTGGAACTAATTTCTCTCAAGAACCTATTGAAAAAGGTTTAGCA
 AAGACTGGTGTTTTAAATATTATCGGAAGTACTGAAGTAAAAAATGAAGCTAAAAATATCA
 AGTCAGACCCAAATTTACTTTAGAAAAAGGTGACAAAAATAATATGATCAAGTATTGACA
 GCAGATGGTTACCAAGTGGATTCTTACAAATCTTATAGTGGTGTTCGTCGTATATTCTCT
 GTGAAAAAGCTAACTACAGTAGTGAAGAAAGCGAAGATGAGGCGACTAAACCGACTAGT
 TATCCCAACTTACCTTAAACAGGTACCTATACATTTACTAAAACCTGATAGTGTGAAAAAGT
 CAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTGAAGAAATACATTAT
 GATCAAGTGTTAGTAGTAGATGGTTCATCAGTGGATTTTATACAAAGAGTTATTCGGTATT
 CGTCGTATATTGAAAT

SEQ ID NO. 8902

STRAIN 090

AAAAAAGGACAAAGTAAATGATACTAAGCAATCTTACT
 CTCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATT
 ATAATGGTCACAAGTCTGTTTGTGCGGATCAAACATACATCGGTTCAAGT
 TAATAATCAGACAGGCCTAGTGTGGATGCTAATAATCTTCCAATGAGA
 CAAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGTCT
 GATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCC
 TTTAGTAGAGACAAAGCCAAATGGTGGAAAAACATTACCTGAACAAGGGA
 ATTATGTTTATAGCAAGAAACCGAGGTGAAAAATACACCTTCAAATCA
 GCCCCAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTCTATGACCA
 AGTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTGTG
 GCGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTCA
 GAGACTAAAGCACCTACTCCTGTAAACAAATTCAGGAAGCAATAATCAAGA
 GAAAAATAGCAACGCAAGGAAATATACATTTTACATAAAGTAGAAGTAA
 AAAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGA
 GACAGAATTTTACGACCAAAATACTAACTATTGAAGGAAATCAGTGGTT
 ATCTTATAAATCAITCAATGGTGTTCGTCGTTTGTCTGCTAGGTAAAG
 CATCTTCAGTAGAAAAAATGAAGATAAAGAAAAAGTGTCTCCTCAACCA
 CAAGCCCGTATTACTAAAACTGGTAGACTGACTATTTCTAACGAAACAA
 TACAGGTTTTGATATTTAATTACGAATATTAAAGATGATAACGGTATCG
 CTGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGCAAGATGATATT
 AAATGGTATACAGCTGTAACTACTGGGGATGGCAACTACAAAGTAGCTGT
 ATCATTTGCTGACCATAAGAATGAGAAGGGTCTTTATAATATTCAITTAT
 ACTACCAAGAGCTAGTGGGACACTTGTAGGTGTAAACAGGAACATAAGTG
 ACAGTAGCTGGAACATAATCTTCTCAAGAACCTATTGAAAAAGGTTTAGC
 AAAGACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAATGAAG
 CTAAAAATATCAAGTCAAGTCAAGCCCAATTTACTTTAGAAAAAGGTGACAAAAATA
 AATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTCTTACAA
 ATCTTATAGTGGTGTTCGTCGCTATATTCCTGTGAAAAAGCTAACTACAA
 GTAGTGAAGAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAAC
 TTACCTAAAAAGGTACCTATACATTTACTAAAACTGTAGATGTGAAGAG
 TCAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTCAAAGGGTGAAG
 AAATACATTATGATCAAGTGTAGTAGTAGATGGTTCATCAGTGGATTTCA
 TACAAGAGTTATTCGGTATTCGTCGCTATATTGAAAT

SEQ ID NO. 8903

STRAIN A909

AAAAAAGGACAAAGTAAATGATACTAAGCAATCTTAC
 TCCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATT
 CATATAAGTCAAGTCTGTTTGTGCGGATCAAACATACATCGGTTCAAG
 TTAATAATCAGACAGGCCTAGTGTGGATGCTAATAATCTTCCAATGAG
 ACAAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGTCT
 TGATAAAGTTGTAATAGTCAAAATACGGCAACAAAGGACATTACTACTC
 CTTTAGTAGAGACAAAGCCATGGTGGAAAAACATTACCTGAACAAGGG
 AATTATGTTTATAGCAAGAAACCGAGGTGAAAAATACACCTTCAAATC
 AGCCCCAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTTCTATGACC
 AAGTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTGT
 GCGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTT
 AGAGACTAAAGCACCTACTCCTGTAAACAAATTCAGGAAGCAATAATCAAG
 AGAAAAATAGCAACGCAAGGAAATTTATACATTTTACATAAAGTAGAAGTA
 AAAAAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGG

Table 89: Comparative Sequences relating to SAG1350

AGACAGAATTTTTTACGACCAAATACTAATCTATTGAAGGAAATCAGTGGT
TATCTTATAAATCATTCAATGGTGTTCGTGTTTTGTTTGCTAGGTAAA
GCATCTTCAGTAGAAAAAAGCTGAAGATAAAGAAAAAGTGTCTCTCAACC
ACAAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACAA
CTACAGGTTTTGATATTTAATTACGAATATTAAGATGATAACGGTATC
GCTGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATAT
TAAATGGTATACAGCTGTAACCTACTGGGATGGCAACTACAAAGTAGCTG
TATCATTGCTGACCATAAGATGAGAAGGGTCTTTATAATATTCAATTA
TACTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACATAAGT
GACAGTAGCTGGAATAATTCTTCTCAAGAACCATTGAAATGGTTTAG
CAAAGACTGGTGTATTATAATATTATCGGAAGTACTGAAGTAAAAATGAA
GCTAAAATATCAAGTCAGACCCCAATTTACTTTAGAAAAAGGTGACAAAAT
AAATTTATGATCAAGTATTGACAGCAGATGGTTACAGTGGATTCTTACA
AATCTTATAGTGGTGTTCGTGCTATATTCTGTGAAAAAGCTAACTACA
AGTAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAA
CTTACCTAAAACAGGTACCTATACATTTACTAAAACCTGTAGATGTGAAGA
GTCACCTAAAAGTATCAAGTCCAGTGGAAATTAATTTTCAAAGGGTGAA
AAAAATACATTATGATCAAGTGTAGTAGATGGTCATCAGTGGATTTC
ATACAAGAGTTATTCCGGTATTCTGTCGTATATTGAAATT

SEQ ID NO. 8904

STRAIN H36B

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACT
CTCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTTC
ATAATGGTCAACAAGTCTGTGTTTTGCGGATCAAACTACATCGGTTCAAGT
TAATAATCAGACAGGCACTAGTGTGGATGATAAATTTCTTCCAATGAGA
CAAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGTCAAGCGTCT
GATAAAGTTGTAATAGTCAAAATACGGCAACAAAGGACATTACTACTCC
TTTAGTAGAGACAAAGCCAATGGTGGAAAAACATTACCTGAACAAGGGA
ATTATGTTTTATAGCAAGAAACCGAGGTGAAAAATACACCTTCAAAATCA
GCCCCAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTTCTATGACCA
AGTATTTAATAAAGATAAATGTGAAATGGATTTCATATAAGTCTTTTTGTG
GCGTACGTCGATACGCAGCTATTGAGTCAGTAGATCCATCAGGAGGTTCA
GAGACTAAAGCACCTACTCTGTAAACAAATTCAGGAAGCAATATCAAGA
GAAAAATAGCAACGCAAGGAAATATACATTTTACATAAAGTAGAAGTAA
AAAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGA
GACAGAATTTTTTACGACCAAACTAATACTATTGAAGGAAATCAGTGGTT
ATCTTATAAATCATTCAATGGTGTTCGTGTTTTGTTTGCTAGGTAAAG
CATCTTCAGTAGAAAAAAGCTGAAGATAAAGAAAAAGTGTCTCTCAACCA
CAAGCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACAAAC
TACAGGTTTTGATATTTAATTACGAATATTAAAGATGATAACGGTATCG
CTGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATT
AAATGGTATACAGCTGTAACCTACTGGGATGGCAACTACAAAGTAGCTGT
ATCATTTGCTGACCATAAGAATGAGAAGGGTCTTTATAATATTCAATTAT
ACTACCAAGAGCTAGTGGGACACTTGTAGGTGTAACAGCACTAAAGTG
ACAGTAGCTGGAACTAATTTCTTCTCAAGAACCTATTGAAAATGGTTTAGC
AAAGACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAATGAAG
CTAAAATATCAAGTCAGACCCCAATTTACTTTAGAAAAAGGTGACAAAATA
AATTATGATCAAGTATTGACAGCAGATGGTTACAGTGGATTTCTTACAA
ATCTTATAGTGGTGTTCGTGCTATATTCTGTGAAAAAGCTAACTACAA
GTAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAAC
TTACCTTAAAACAGGTACCTATACATTTACTAAAACCTGTAGATGTGAAGAG
TCAACCTTAAAGTATCAAGTCCAGTGGAAATTAATTTTCAAAGGGTGAAA
AAATACATTATGATCAAGTGTAGTAGTAGATGGTCATCAGTGGATTTC
TACAAGAGTTATTCCGGTATTCTGTCGTATATTGAAATT

SEQ ID NO. 8905

STRAIN 18RS21

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACTC
TCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTCA
TAATGGTCAACAAGTCTGTGTTTTGCGGATCAAACTACATCGGTTCAAGTT
AATAATCAGACAGGCACTAGTGTGGATGCTAATAATTTCTTCCAATGAGAC
AAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGTCAAGCGTCTG
ATAAAGTTGTAATAAGTCAAAATACGGCAACAAAGGACATTACTACTCT
TTAGTAGAGACAAAGCCAATGGTGGAAAAACATTACCTGAACAGGGAA
TTATGTTTATAGCAAGAAACCGAGGTGAAAAATACACCTTCAAAATCAG
CCCCAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTTCTATGACCAA
GTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTTGTGG
CGTAGCTGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTGAG
AGACTAAAGCACCTACTCTGTAAACAAATTCAGGAAGCAATAATCAAGAG
AAAATAGCAACGCAAGGAAATATACATTTTACATAAAGTAGAAGTAAA
AAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGCAAAAGGAG
ACAGAATTTTTTACGACCAAACTAATACTATTGAAGGAAATCAGTGGTTA
TCTTATAAATCATTCAATGGTGTTCGTGTTTTGTTTGCTAGGTAAAGC
ATCTTCAGTAGAAAAAAGCTGAAGATAAAGAAAAAGTGTCTCTCAACCAC
AAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACAACT
ACAGGTTTTGATATTTAATTACGAATATTAAAGATGATAACGGTATCGC
TGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATTA
AATGGTATACAGCTGTAACCTACTGGGATGGCAACTACAAAGTAGCTGTA
TCATTTGCTGACCATAAAGATGAGAAGGGTCTTTATAATATTCAATTTATA
CTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACATAAGTGA
CAGTAGCTGGAACATAATTTCTTCAAGAACCTATTGAAAAAGGTTTAGCA
AAGACTGGTGTATTATAATATTATCGGAAGTACTGAAGTAAAAATGAAGC

Table 89: Comparative Sequences relating to SAG1350

TAAATATCAAGTCAGACCCCAATTTACTTTAGAAAAAGGTGACAAAATAA
 ATTATGATCAAGTATTGACAGCAGATGGTTACCAAGTGGATTTCTTACAAA
 TCTTATAGTGGTGTTCGTCGTATATTCCTGTGAAAAAGCTAACTACAAG
 TAGTGA AAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAACT
 TACCTAAAACAGGTACCTATACATTTACTAAAACGTAGATGTGAAAAGT
 CAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAAGGGTGAAAA
 AATACATTATGATCAAGTGTAGTAGTAGATGGTCATCAGTGGATTTTCAT
 ACAAGAGTTATTCCGGTATTTCGTTCGTATATTGAAATT

SEQ ID NO. 8906

STRAIN M732

CAAGTAAATGATaCTAAGCAATCTTACTCTCTACGTAAATATAAATTGG
 TTTAGCATCAGTAATTTTAGGGTCATTTCATAATGGTCACAAGTCCGTGTT
 TTGCGGATCAAAcTACATCGGTTCAAGTTAATAATCAGACAGGCACTAGT
 GTGGATGCTAATAATTCTTCCAATGAGACAAGTCCGTCAAGTGTGATTAC
 TTCCAATATGATAGTGTTCAGCGCTCGATAAAGTTGTAAATAGTCAAA
 ATACGGCAACAAAGGACATTACTACTCCTTTAGTAGAGACAAGCCAATG
 GTGGA AAAACATTTACCTGAACAAGGGAATTATGTTTATAGCAAGA AAC
 CGAGGTGAAAAATACACCTTCAAAATCAGCCCCAGTAGCTTTCTATGCAA
 AGAAAGGTGATAAAGTTTCTATGACCAAGTATTTAATAAAGATAATGTG
 AAATGGATTT CATATAAGTCTTTTGGTGGCGTACGTTCGATACGCAGCTAT
 TGAGTCACTAGATCCATCAGGAGGTTTCAGAGACTAAAGCACCTACTCCTG
 TAACAAATTCAGGAAGCAATAATCAAGAGAAAAATAGCAACGCAAGGAAT
 TATACATTTTACATAAAGTAGAAGTAAAAATGAAGCTAAGGTAGCGAG
 TCCAATCAATTTTACATTGGACAAAGGAGACAGAATTTTACGACCAAA
 TACTAACTatTGAAGGAATCAGTGGTTATCTTATAAATCATTCATGGT
 GTTCGTCTGTTTGTtTtGcTAGGTAAGCATCTTCAGTAGAAAAAACTGA
 AGATAAAGAAAAAGTGTCTCCTCAACCACAAGCCGTATTACTAAAACCTG
 GTAGACTGACTATTTCTAACGAAACAACTACAGGTTTGTATATTTAATT
 ACGAATATTAAGATGATAACGGTATCGCTGCTGTTAAGGTACCGGTTTG
 GACTGAACAGGAGGCGCAAGATGATATTAATGGTATACAGCTGTAACATA
 CTGGGGATGGCAACTACAAAGTAGCTGTATCATTTGCTGACCATAGAAT
 GAGAAGGGTCTTTATAATATTCAATTATATCTACCAAGAAGCTAGTGGGAC
 ACTTGTAGGTGTAACAGGAACATAAGTGACAGTAGCTGGAACATAATCTT
 CTCAGAAGACCTATTGAAAATGGTTTACCAAGACTGGTGTTTATAATATT
 ATCGGAAGTACTGAAGTAAAAAATGAAGCTAAAAATATCAAGTCAGACCCA
 ATTTACTTTAGAAAAAGGTGACAAAAATAAATTATGATCAAGTATTGACAG
 CAGATGGTTTACCAAGTGGATTTCTTACAAATCTTATAGTGGTGTTCGTGCG
 TATATTCTGTGAAAAAGCTAACTACAAGTAGTGA AAAAGCGAAAGATGA
 GGCGACTAAACCGACTAGTTATCCCAACTTACCTAAACAGGTACCTATA
 CATTTACTAAAACGTAGATGTGAAAAGTCAACCTAAAGTATCAAGTCCA
 GTGGAATTTAATTTTCAAAAGGGTGAAAAATACATTATGATCAAGTGT
 AGTAGTAGATGGTCATCAGTGGATTTCATACAAAGATTATTCCGGTATTC
 GTCGTATATTGAAATT

SEQ ID NO. 8907

STRAIN COH1

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACTCTCT
 ACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTTCATAA
 TGGTCACAAGTCCGTGTTTTCGCGGATCAAACTACATCGGTTCAAGTTAAT
 AATCAGACAGGCACTAGTGTGGATGCTAATAATCTTCCAATGAGACAAG
 TGCGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGTCTGATA
 AAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCCTTTA
 GTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAAGGAATTA
 TGTTTATAGCAAAAGAACCGAGGTGAAAAATACACCTTCAAAATCAGCCC
 CAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTCTATGACCAAGTA
 TTTAATAAAGATAATGTTAAATGGATTTCATATAAGTCTTTTGGTGGCGT
 ACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTTCAGAGA
 CTAAGCACCTACTCTGTAAACAAATTCAGGAAGCAATAATCAAGAGAAA
 ATAGCAACGCAAGGAAATATACATTTTCACATAAAGTAGAAGTAaaaaa
 TGAAGcTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAGGAGACA
 GAATTTTTTACGACCAATACTAATCTATTGAAGGAAATCAGTGGTTATCT
 TATAAATCATTCATGGTGTTCGTGCTTTTGTtTGCTAGGTAAAGCATC
 TTCAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCTCAACCACAAG
 CCCGTTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACAACTACA
 GGTTTTGATATTTTAATTACGAATATTAAAGATGATAACGGTATCGCTGC
 TGTTAAGGTACCGGTTTGGACTGAACAAGGAGGCAAGATGATATTAAAT
 GGTATACAGCTGTAACTACTGGGGATGGCAACTACAAAGTAGCTGTATCA
 TTTGCTGACCATAGAATGAGAAGGGTCTTTATAATATTCAATTATACTA
 CCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACATAAGTGACAG
 TAGCTGGAACATAATCTTCTCAAGAACCTATTGAAAAAGGTTTACCAAG
 ACTGGTGTTTATAATATATCGGAAGTACTGAAGTAAAAAATGAAGCTAA
 AATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAATAAAT
 ATGATCAAGTATTGACAGCAGATGGTTACCAAGTGGATTCTTACAAATCT
 TATAGTGGTGTTCGTGCTATATTCTGTGAAAAAGCTAACTACAAGTAG
 TGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAACTTAC
 CTAAAACAGGTACCTATACATTTACTAAAACGTAGATGTGAAAAGTCAA
 CCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAAGGGTGAAAAAT
 ACATTATGATCAAGTGTAGTAGTAGATGGTCATCAGTGGATTTCATACA
 AGAGTTATTCCGGTATTTCGTGCTATATTGAAATT

SEQ ID NO. 8908

STRAIN M781

Table 89: Comparative Sequences relating to SAG1350

AAAAAAGGACAAAGTAAATGATACTAAGCAATCTT
 ACTCTCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCA
 TTCATAATGGTCAACAAGTCCTGTTTTTGGGATCAAACCTACATCGGTTCA
 AGTTAATAATCAGACAGGCACTAGTGTGGATGCTAATAATTTCTCCAATG
 AGACAAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGTCAAGCG
 TCTGATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTAC
 TCCTTTAGTAGAGACAAAGCCAATGGTGGAAAAACATTACCTGAACAAG
 GGAATTATGTTTATAGCAAAAGAAACCGAGGTGAAAAATACACCTTCAAAA
 TCAGCCCCAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTCTATGA
 CCAAGTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTG
 GTGGCGTACGTGATACGACGCTATTGAGTCACTAGATCCATCAGGAGGT
 TCAGAGACTAAAGCACCTACTCTGTAAACAAATTCAGGAAGCAATAATCA
 AGAGAAAATAGCAACGCAAGGAAATATACATTTTCACTATAAGTAGAAG
 TAAAAAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAA
 GGAGACAGAAATTTTACGACCAAACTACTAATTTGAAGGAAATCAGTG
 GTTATCTTATAAATCATTTCAATGGTGTTCGTCGTTTTGTTTGTCTAGGTA
 AAGCATCTTCAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCCTCAA
 CCACAAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAAC
 AACTACAGGTTTTGATATTTAATTACGAATATTAAAGATGATAACGGTA
 TCGCTGCTGTTAAGGTACCGGTTTGGACTGAACAGGAGGGCAAGATGAT
 ATTAATGGTATACAGCTGTAACTACTGGGGATGGCACTACAAAGTAGC
 TGTATCATTTGCTGACCATAGAATGAGAAGGGTCTTTATAATATTCAATT
 TATACACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACATAA
 GTGACAGTAGCTGGAACTAATTCTTCTCAAGAACCTATTGAAATGGTTT
 ACCAAAGACTGGTGTATATAATATTATCGGAAGTACTGAAGTAAAAATG
 AAGCTAAAAATATCAAGTCAAGCCAAATTTACTTTAGAAAAAGGTGACAAA
 ATAAATTTAGTATCAAGTATTGACAGCAGATGGTTACCAAGTGGATTTCTTA
 CAAATCTTATAGTGGTGTTCGTCGTATATTTCTGTGAAAAAGCTAACTA
 CAAGTAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCC
 AACTTACCTAAAAACAGGTACCTATACATTTTACTAAAACTGTAGATGTGAA
 AAGTCAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTG
 AAAAAATACATTATGATCAAGTGTAGTAGTAGATGGTCACTAGTGGATT
 TCATACAAGAGTTATTCGGGTATTTCGTCGTATATTGAAATT

SEQ ID NO. 8909

STRAIN CJB110

AAAAAAGGACAAAGTAAATGATACTAAGCAATCTTACTCTC
 TACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTATA
 ATGGTCAACAAGTCCTGTTTTTGGGATCAAACCTACATCGGTTCAAGTTAA
 TAATCAGACAGGCACTAGTGTGGATGCTAATAATTTCTTCCAATGAGACAA
 GTGCGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGCTGTAT
 AAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCCTTT
 AGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAAGGGAAT
 ATGTTTATAGCAAGAAACCGAGGTGAAAAATACACCTTCAAAATCAGCC
 CCAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTTCTATGACCAAGT
 ATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTTGTGGCG
 TACGTGATACGACGCTATTGAGTCACTAGATCCATCAGGAGGTTTCAGAG
 ACTAAAGCACCTACTCCTGTAAACAAATTCAGGAAGCAATAATCAAGAGAA
 AATAGCAACGCAAGGAAATATACATTTTCACTATAAAGTAGAAGTAAAAA
 ATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGAGAC
 AGAATTTTTACGACCAATACTAATTTGAAGGAAATCAGTGGTTATC
 TTATAAATCATTTCAATGGTGTTCGTCGTTTTGTTTGTCTAGGTAAAGCAT
 CTTCAAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCCTCAACCCAA
 GCCCGTATTACTAAACCTGGTAGACTGACTATTTCTAACGAAACCACTAC
 AGGTTTTGATATTTAATTACGAATATTAAAGATGATAACGGTATCGCTG
 CTGTTAAGGTACCGGTTTGGACTGAACAGGAGGGCAAGATGATATTA
 TGGTATACAGCTGTAACCTAGTGGGATGGCAACTACAAAGTAGCTGTATC
 ATTTGCTGACCATAGAATGAGAAGGGTCTTTATAATATTCAATTTACT
 ACCAAGAAGCTAGTGGGACACTTGTAGGTGTACAGGAACATAAGTGACA
 GTAGCTGGAACATAATCTTCTCAAGAACCTATTGAAATGGTTTAGCAAA
 GACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAATGAAGCTA
 AAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAATAAAT
 TATGATCAAGTATTGACAGCAGATGGTTACCAAGTGGATTCTTACAAATC
 TTATAGTGGTGTTCGTCGCTATATTCTGTGAAAAAGCTAACTACAAAGTA
 GTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAACTTA
 CCTAAACAGGTACCTATACATTTACTAAACCTGTAGATGTGAAGAGTCA
 ACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTGAAAAAA
 TACATTATGATCAAGTGTAGTAGTAGATGGTCACTAGTGGATTTCATAC
 AAGAGTTATTCGGGTATTTCGTCGCTATATTGAAATT

SEQ ID NO. 8910

STRAIN 1169NT

AAAAAAGGACAAAGTAAATGATACTAAGCAATCTTACTC
 TCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTCA
 TAATGGTCAACAAGTCCTGTTTTTGGGATCAAACCTACATCGGTTCAAGTT
 AATAATCAGACAGGCACTAGTGTGGATGCTAATAATTTCTTCCAATGAGAC
 AAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGCTGTG
 ATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCCT
 TTAGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAAGGAA
 TTATGTTTATAGCAAGAAACCGAGGTGAAAAATACACCTTCAAAATCAG
 CCCAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTTCTATGACCAA
 GTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTGGTGG
 CGTACGTGATACGACGCTATTGAGTCACTAGATCCATCAGGAGGTTTCAG

Table 89: Comparative Sequences relating to SAG1350

AGACTAAAGCACCTACTCCTGTAAACAAATTCAGGAAGCAATAATCAAGAG
 AAAATAGCAACGCAAGGAAATTTATACATTTTCACATAAAGTAGAAGTAAA
 AAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGAG
 ACAGAATTTTACGACCAATATACTAATTTGAAGGAAATCAGTGGTTA
 TCTTATAAATCAATCAATGGTGTTCGTGTTTTGTTTTGCTAGGTAAAGC
 ATCTTCAGTAGAAAAAAGTGAAGATAAAGAAAAAGTGTCTCTCAACCAC
 AAGCCCGTATTACTAAACTGGTAGACTGACTATTTCTAACGAAACCACT
 ACAGGTTTTGATATTTAATTACGAATATTAAGATGATAACGGTATCGC
 TGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGCAAGATGATATTA
 AATGGTATACAGCTGTAACACTGGGGATGGCAACTACAAAGTAGCTGTA
 TCATTTGCTGACCATAGAATGAGAAGGGTCTTTATAATATTCATTTATA
 CTACCAAGAGCTAGTGGGACACTTGTAGGTGTAACAGGAACATAAGTGA
 CAGTAGCTGGAaCTAATCTCTCAAGAACCTATTGAAAAAGGTTTAGCA
 AAGACTGGTGTATTATAATATTATCGGAAGTACTGAAGTAAAAATGAAGC
 TAAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAATAA
 ATTATGATCAAGTATTGACAGCAGATGGTTACCACTGGATTCTTTACAAA
 TCTTATAGTGGTGTTCGTGCTATATTCTGTGAAAAAGCTAACTACAAG
 TAGTGA AAAAGCGAAGATGAGGCGACTAAACCGACTAGTTATCCCACT
 TACCTAAACAGGTACCTATACATTTACTAAAAGTGTAGATGTGAAAAAGT
 CAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTGAAAA
 AATACATTATGATCAAGTGTAGTAGTAGTGGTCATCAGTGGATTTCAT
 ACAAGAGTTATTCCGGTATTCTGCTGCTATATTGAAATT

SEQ ID NO. 8911

STRAIN JM9130013

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACT
 CTCTACGTAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTC
 ATAATGGTCACAAGTCTGTTTTTGCGGATCAAACTACATCGGTTCAAGT
 TAATAATCAGACAGGCAGTGTGGATGCTAATAATTTCTTCAATGAGA
 CAAGTGCCTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGTCT
 GATAAAGTTGTAATAGTCAAAATACGGCAACAAAGGACATTACTACTCC
 TTTAGTAGAGACAAAGCCAATGGTGGAAAAACATTAACCTGAACAAGGGA
 ATTATGTTTATAGCAAAAGAACCGAGGTGAAAAATACACCTTCAAATCA
 GCCCAGTAGCTTTCTATGCAAAAGAGGTGATAAAGTTTTCTATGACCA
 AGTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTGTG
 GCGTACGTCGATACGAGCTATTGAGTCACTAGATCCATCAGGAGGTTCA
 GAGACTAAAGCACCTACTCTCTGTAACAAATTCAGGAAGCAATAATCAAGA
 GAAATAGCAACGCAAGGAAATTTATACATTTTTCACATAAAGTAGAAGTAA
 AAAATGAAGCTAAGGTAGCGAGTCCAACTCAATTTACATTGGACAAAGGA
 GACAGAATTTTTTACGACCAAAATACTAATTTGAAGGAAATCAGTGGTT
 ATCTTATAAATCATTCATGGTGTTCGTGTTTTGTTTTGCTAGGTAAAG
 CATCTTCAGTAGAAAAAAGTGAAGATAAAGAAAAAGTGTCTCCTCAACCA
 CAAGCCCGTATTACTAAAAGTGGTAGACTGACTATTTATAACGAAACCAAC
 TACAGGTTTTGATATTTAATTACGAATATAAAGATGATAACGGTATCG
 CTGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATT
 AAATGGTATACAGCTGTAACACTCTGGGATGGCAACTACAAAGTAGCTGT
 ATCATTTGCTGACCATAGAATGAGAAGGGTCTTTATAATATTCATTTAT
 ACTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACATAAGTG
 ACAGTAGCTGGAACTAATTTCTCTCAAGAACCTATTGAAAAAGGTTTAGC
 AAAGACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAAATGAAG
 CTAAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAATA
 AATTATGATCAAGTATTGACAGCAGATGGTTACCACTGGATTCTTTACAA
 ATCTTATAGTGGTGTTCGTGCTATATTCTGTGAAAAAGCTAACTACAA
 GTAGTGAAAAAGCGAAGATGAGGCGACTAAACCGACTAGTTATCCCAAC
 TTACCTAAAACAGGTACCTATACATTTACTAAAAGTGTAGATGTGAAGAG
 TCAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTGAAA
 AAATACATTATGATCAAGTGTAGTAGTAGTGGTCATCAGTGGATTTCAT
 TACAAGAGTTATTCCGGTATTCTGCTGCTATATTGAAATT

PRETTY of: /biotmp/msa255059.2{*} February 11, 2003 08:41 ..

	1		50
msa255059.2{91_M732}	-----	--CAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_M781}	---AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_COH1}	---AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_18RS21}	---AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_2603}	atgAAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_1169NT}	---AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_090}	---AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_A909}	---AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_CJB110}	---AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_H36B}	---AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_JM9130013}	---AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
Consensus	*****	*****	*****

	51		100
msa255059.2{91_M732}	ATATAAATTT	GGTTAGCAT	CAGTAATTTT AGGGTCATTC ATAATGGTCA
msa255059.2{91_M781}	ATATAAATTT	GGTTAGCAT	CAGTAATTTT AGGGTCATTC ATAATGGTCA
msa255059.2{91_COH1}	ATATAAATTT	GGTTAGCAT	CAGTAATTTT AGGGTCATTC ATAATGGTCA
msa255059.2{91_18RS21}	ATATAAATTT	GGTTAGCAT	CAGTAATTTT AGGGTCATTC ATAATGGTCA
msa255059.2{91_2603}	ATATAAATTT	GGTTAGCAT	CAGTAATTTT AGGGTCATTC ATAATGGTCA
msa255059.2{91_1169NT}	ATATAAATTT	GGTTAGCAT	CAGTAATTTT AGGGTCATTC ATAATGGTCA

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_090}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_A909}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_CJB110}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_H36B}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_JM9130013}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_M781}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_COH1}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_18RS21}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_2603}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_1169NT}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_090}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_A909}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_CJB110}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_H36B}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_JM9130013}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_M781}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_COH1}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_18RS21}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_2603}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_1169NT}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_090}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_A909}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_CJB110}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_H36B}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_JM9130013}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_M781}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_COH1}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_18RS21}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_2603}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_1169NT}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_090}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_A909}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_CJB110}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_H36B}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_JM9130013}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_M781}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_COH1}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_18RS21}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_2603}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_1169NT}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_090}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_A909}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_CJB110}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_H36B}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_JM9130013}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_M781}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_COH1}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_18RS21}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_2603}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_1169NT}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_090}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_A909}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_CJB110}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_H36B}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_JM9130013}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_M781}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_COH1}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_18RS21}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_2603}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_1169NT}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_090}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_A909}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_CJB110}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_H36B}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_JM9130013}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
Consensus	*****	*****	*****	*****	*****
401	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_M732}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_M781}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_COH1}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_18RS21}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_2603}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_1169NT}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_090}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_A909}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_CJB110}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_H36B}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_JM9130013}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
Consensus	*****	*****	*****	*****	*****
451	AAAGATAATG	TgAAATGGAT	TTTATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_M732}	AAAGATAATG	TgAAATGGAT	TTTATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_M781}	AAAGATAATG	TgAAATGGAT	TTTATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_COH1}	AAAGATAATG	TgAAATGGAT	TTTATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_18RS21}	AAAGATAATG	TgAAATGGAT	TTTATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_2603}	AAAGATAATG	TgAAATGGAT	TTTATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_1169NT}	AAAGATAATG	TgAAATGGAT	TTTATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_090}	AAAGATAATG	TgAAATGGAT	TTTATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_A909}	AAAGATAATG	TgAAATGGAT	TTTATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_CJB110}	AAAGATAATG	TgAAATGGAT	TTTATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_H36B}	AAAGATAATG	TgAAATGGAT	TTTATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_JM9130013}	AAAGATAATG	TgAAATGGAT	TTTATATAAG	TCTTTTgGTG	GCGTACGTCG
Consensus	*****	*..*****	*****	*****_***	*****
501	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_M732}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_M781}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_COH1}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_18RS21}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_2603}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_1169NT}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_090}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_A909}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_CJB110}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_H36B}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_JM9130013}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
Consensus	*****	*****	*****	*****	*****
551	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_M732}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_M781}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_COH1}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_18RS21}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_2603}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_1169NT}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_090}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_A909}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_CJB110}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_H36B}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_JM9130013}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
Consensus	*****	*****	*****	*****	*****
601	ACGCAAGGAA	ATTATACATT	TTTACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_M732}	ACGCAAGGAA	ATTATACATT	TTTACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_M781}	ACGCAAGGAA	ATTATACATT	TTTACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_COH1}	ACGCAAGGAA	ATTATACATT	TTTACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_18RS21}	ACGCAAGGAA	ATTATACATT	TTTACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_2603}	ACGCAAGGAA	ATTATACATT	TTTACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_1169NT}	ACGCAAGGAA	ATTATACATT	TTTACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_090}	ACGCAAGGAA	ATTATACATT	TTTACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_A909}	ACGCAAGGAA	ATTATACATT	TTTACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_CJB110}	ACGCAAGGAA	ATTATACATT	TTTACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_H36B}	ACGCAAGGAA	ATTATACATT	TTTACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_JM9130013}	ACGCAAGGAA	ATTATACATT	TTTACATAAA	GTAGAAGTAA	AAAATGAAGC
Consensus	*****	*****	*****	*****	*****
651	TAAGGTAGCG	AGTCCAATC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_M732}	TAAGGTAGCG	AGTCCAATC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_M781}	TAAGGTAGCG	AGTCCAATC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_COH1}	TAAGGTAGCG	AGTCCAATC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_18RS21}	TAAGGTAGCG	AGTCCAATC	AATTTACATT	GGACAAAGGA	GACAGAATTT

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_2603}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_1169NT}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_090}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_A909}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_CJB110}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_H36B}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_JM9130013}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_M781}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_COH1}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_18RS21}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_2603}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_1169NT}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_090}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_A909}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_CJB110}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_H36B}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_JM9130013}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_M781}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_COH1}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_18RS21}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_2603}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_1169NT}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_090}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_A909}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_CJB110}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_H36B}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_JM9130013}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	AGAAAAAAGT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_M781}	AGAAAAAAGT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_COH1}	AGAAAAAAGT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_18RS21}	AGAAAAAAGT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_2603}	AGAAAAAAGT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_1169NT}	AGAAAAAAGT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_090}	AGAAAAAAGT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_A909}	AGAAAAAAGT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_CJB110}	AGAAAAAAGT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_H36B}	AGAAAAAAGT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_JM9130013}	AGAAAAAAGT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_M781}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_COH1}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_18RS21}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_2603}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_1169NT}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_090}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_A909}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_CJB110}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_H36B}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_JM9130013}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
Consensus	*****	*****	*****-*	*****	*****
msa255059.2{91_M732}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_M781}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_COH1}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_18RS21}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_2603}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_1169NT}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_090}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_A909}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_CJB110}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_H36B}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_JM9130013}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_M781}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_COH1}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_18RS21}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_2603}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_1169NT}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_090}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_A909}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_CJB110}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_H36B}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_JM9130013}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_M781}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_COH1}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_18RS21}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_2603}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_1169NT}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_090}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_A909}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_CJB110}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_H36B}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_JM9130013}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_M781}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_COH1}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_18RS21}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_2603}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_1169NT}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_090}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_A909}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_CJB110}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_H36B}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_JM9130013}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_M781}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_COH1}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_18RS21}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_2603}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_1169NT}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_090}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_A909}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_CJB110}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_H36B}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_JM9130013}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_M781}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_COH1}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_18RS21}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_2603}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_1169NT}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_090}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_A909}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_CJB110}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_H36B}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_JM9130013}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_M781}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_COH1}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_18RS21}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_2603}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_1169NT}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_090}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_A909}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_CJB110}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_H36B}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_JM9130013}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_M781}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC

msa255059.2{91_COH1}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC	
msa255059.2{91_18RS21}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC	
msa255059.2{91_2603}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC	
msa255059.2{91_1169NT}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC	
msa255059.2{91_A909}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC	
msa255059.2{91_CJB110}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC	
msa255059.2{91_H36B}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC	
msa255059.2{91_JM9130013}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC	
Consensus	*****	*****	*****	*****	*****	
msa255059.2{91_M732}	1301	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_M781}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_COH1}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_18RS21}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_2603}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_1169NT}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_A909}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_CJB110}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_H36B}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_JM9130013}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
Consensus	*****	*****	*****	*****	*****	*****
msa255059.2{91_M732}	1351	GGTGTTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAAA
msa255059.2{91_M781}	GGTGTTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAAA	GTAGTGAAAA
msa255059.2{91_COH1}	GGTGTTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAAA	GTAGTGAAAA
msa255059.2{91_18RS21}	GGTGTTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAAA	GTAGTGAAAA
msa255059.2{91_2603}	GGTGTTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAAA	GTAGTGAAAA
msa255059.2{91_1169NT}	GGTGTTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAAA	GTAGTGAAAA
msa255059.2{91_A909}	GGTGTTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAAA	GTAGTGAAAA
msa255059.2{91_CJB110}	GGTGTTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAAA	GTAGTGAAAA
msa255059.2{91_H36B}	GGTGTTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAAA	GTAGTGAAAA
msa255059.2{91_JM9130013}	GGTGTTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAAA	GTAGTGAAAA
Consensus	*****	*****	*****	*****	*****	*****
msa255059.2{91_M732}	1401	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_M781}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_COH1}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_18RS21}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_2603}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_1169NT}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_A909}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_CJB110}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_H36B}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_JM9130013}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
Consensus	*****	*****	*****	*****	*****	*****
msa255059.2{91_M732}	1451	CAGGTACCTA	TACATTTACT	AAAACGTGAG	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_M781}	CAGGTACCTA	TACATTTACT	AAAACGTGAG	AAAACGTGAG	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_COH1}	CAGGTACCTA	TACATTTACT	AAAACGTGAG	AAAACGTGAG	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_18RS21}	CAGGTACCTA	TACATTTACT	AAAACGTGAG	AAAACGTGAG	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_2603}	CAGGTACCTA	TACATTTACT	AAAACGTGAG	AAAACGTGAG	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_1169NT}	CAGGTACCTA	TACATTTACT	AAAACGTGAG	AAAACGTGAG	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_A909}	CAGGTACCTA	TACATTTACT	AAAACGTGAG	AAAACGTGAG	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_CJB110}	CAGGTACCTA	TAC				

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_M781}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTTC	TACAAGAGTT
msa255059.2{91_COH1}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTTC	TACAAGAGTT
msa255059.2{91_18RS21}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTTC	TACAAGAGTT
msa255059.2{91_2603}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTTC	TACAAGAGTT
msa255059.2{91_1169NT}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTTC	TACAAGAGTT
msa255059.2{91_090}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTTC	TACAAGAGTT
msa255059.2{91_A909}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTTC	TACAAGAGTT
msa255059.2{91_CJB110}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTTC	TACAAGAGTT
msa255059.2{91_H36B}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTTC	TACAAGAGTT
msa255059.2{91_JM9130013}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTTC	TACAAGAGTT
Consensus	*****	*****	*****	*****	*****

	1601		1629
msa255059.2{91_M732}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_M781}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_COH1}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_18RS21}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_2603}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_1169NT}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_090}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_A909}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_CJB110}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_H36B}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_JM9130013}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
Consensus	*****	*****	*****

SEQ ID NO. 8912

STRAIN 2603 frame: 1

MKKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSPPVFADQTTTSVQVNNQGTGSVDANNSS
 SNETSASSVITSNNDVSVQASDKVNVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYYSKE
 TEVKNTPSKSAPVAFYAKKGDVVFYDQVFNKDNVNWISYKSFVCGVRRYAAIESLDPSGGSS
 ETKAPTPTVNSGNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFDYDQILTI
 IEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGTDGNYKVAVSFADHKNEKGLYNI
 IHLYYQEASGTLVGVTGKVTVAGTNSSQEPIENGLAKTGNYNIIGSTEVEKNEAKISSQTQ
 FTLEKGDKNINYDQVLTDAGYQWISYKSYSGVRRYIPVKKLTTSSSEKAKDEATKPTSYPNL
 PKTGTYYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVDGHWISYKSYSGIRRYI
 EI

SEQ ID NO. 8913

STRAIN 090 frame: 1

KKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSPPVFADQTTTSVQVNNQGTGSVDANNSS
 NETSASSVITSNNDVSVQASDKVNVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYYSKET
 EVKNTPSKSAPVAFYAKKGDVVFYDQVFNKDNVNWISYKSFVCGVRRYAAIESLDPSGGSE
 TKAPTPTVNSGNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFDYDQILTI
 IEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGTDGNYKVAVSFADHKNEKGLYNI
 HLYYYQEASGTLVGVTGKVTVAGTNSSQEPIENGLAKTGNYNIIGSTEVEKNEAKISSQTQ
 FTLEKGDKNINYDQVLTDAGYQWISYKSYSGVRRYIPVKKLTTSSSEKAKDEATKPTSYPNL
 PKTGTYYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVDGHWISYKSYSGIRRYI
 EI

SEQ ID NO. 8914

STRAIN A909 frame: 1

KKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSPPVFADQTTTSVQVNNQGTGSVDANNSS
 NETSASSVITSNNDVSVQASDKVNVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYYSKET
 EVKNTPSKSAPVAFYAKKGDVVFYDQVFNKDNVNWISYKSFVCGVRRYAAIESLDPSGGSE
 TKAPTPTVNSGNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFDYDQILTI
 IEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGTDGNYKVAVSFADHKNEKGLYNI
 HLYYYQEASGTLVGVTGKVTVAGTNSSQEPIENGLAKTGNYNIIGSTEVEKNEAKISSQTQ
 FTLEKGDKNINYDQVLTDAGYQWISYKSYSGVRRYIPVKKLTTSSSEKAKDEATKPTSYPNL
 PKTGTYYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVDGHWISYKSYSGIRRYI
 EI

SEQ ID NO. 8915

STRAIN H36B frame: 1

KKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSPPVFADQTTTSVQVNNQGTGSVDANNSS
 NETSASSVITSNNDVSVQASDKVNVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYYSKET
 EVKNTPSKSAPVAFYAKKGDVVFYDQVFNKDNVNWISYKSFVCGVRRYAAIESLDPSGGSE
 TKAPTPTVNSGNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFDYDQILTI
 IEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGTDGNYKVAVSFADHKNEKGLYNI
 HLYYYQEASGTLVGVTGKVTVAGTNSSQEPIENGLAKTGNYNIIGSTEVEKNEAKISSQTQ
 FTLEKGDKNINYDQVLTDAGYQWISYKSYSGVRRYIPVKKLTTSSSEKAKDEATKPTSYPNL
 PKTGTYYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVDGHWISYKSYSGIRRYI
 EI

SEQ ID NO. 8916

STRAIN 18RS21 frame: 1

KKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSPPVFADQTTTSVQVNNQGTGSVDANNSS
 NETSASSVITSNNDVSVQASDKVNVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYYSKET

Table 89: Comparative Sequences relating to SAG1350

EVKNTPSKSAPVAFYAKKGDKVFDQVFNKDNVWKWISYKSFVGVRRYAAIESLDPSSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIDKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNVYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGKVTVAGTNSSQEPINENGLAKTGNYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINVDQVLTADGYQWISYKSYSGVRRYIPVKKLITSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8917

STRAIN M732 frame: 1

QVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSSNET
SASSVITSNNDSVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKETEVK
NTPSKSAPVAFYAKKGDKVFDQVFNKDNVWKWISYKSFVGVRRYAAIESLDPSSGGSETKA
PTPTVNTSGSNNOEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIDKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNVYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGKVTVAGTNSSQEPINENGLAKTGNYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINVDQVLTADGYQWISYKSYSGVRRYIPVKKLITSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8918

STRAIN COH1 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
EVKNTPSKSAPVAFYAKKGDKVFDQVFNKDNVWKWISYKSFVGVRRYAAIESLDPSSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIDKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNVYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGKVTVAGTNSSQEPINENGLAKTGNYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINVDQVLTADGYQWISYKSYSGVRRYIPVKKLITSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8919

STRAIN M781 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
EVKNTPSKSAPVAFYAKKGDKVFDQVFNKDNVWKWISYKSFVGVRRYAAIESLDPSSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIDKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNVYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGKVTVAGTNSSQEPINENGLAKTGNYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINVDQVLTADGYQWISYKSYSGVRRYIPVKKLITSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8920

STRAIN CJB110 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
EVKNTPSKSAPVAFYAKKGDKVFDQVFNKDNVWKWISYKSFVGVRRYAAIESLDPSSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIDKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNVYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGKVTVAGTNSSQEPINENGLAKTGNYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINVDQVLTADGYQWISYKSYSGVRRYIPVKKLITSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8921

STRAIN 1169NT frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
EVKNTPSKSAPVAFYAKKGDKVFDQVFNKDNVWKWISYKSFVGVRRYAAIESLDPSSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIDKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNVYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGKVTVAGTNSSQEPINENGLAKTGNYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINVDQVLTADGYQWISYKSYSGVRRYIPVKKLITSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8922

STRAIN JM9130013 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
EVKNTPSKSAPVAFYAKKGDKVFDQVFNKDNVWKWISYKSFVGVRRYAAIESLDPSSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIDKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNVYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGKVTVAGTNSSQEPINENGLAKTGNYNIIGSTEVKNEAKISSQTQ

Table 89: Comparative Sequences relating to SAG1350

FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYYTFTKTVDKVSQPKVSSPFVEFNFQKGEKIHYDQVLVVDGHWISYKSYSGIRRYI
EI

PRETTY of: /biotmp/msa255178.2{*} February 11, 2003 08:51 ..

	1				50
msa255178.2{91_090}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_18RS21}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_2603}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_A909}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_CJB110}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_H36B}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_JM9130013}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_COH1}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_M781}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_M732}	----QVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_1169NT}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
Consensus	*****	*****	*****	*****	*****
	51				100
msa255178.2{91_090}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_18RS21}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_2603}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_A909}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_CJB110}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_H36B}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_JM9130013}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_COH1}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_M781}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_M732}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_1169NT}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
Consensus	*****	*****	*****	*****	*****
	101				150
msa255178.2{91_090}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_18RS21}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_2603}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_A909}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_CJB110}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_H36B}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_JM9130013}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_COH1}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_M781}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_M732}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_1169NT}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
Consensus	*****	*****	*****	*****	*****
	151				200
msa255178.2{91_090}	KDNVWKISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_18RS21}	KDNVWKISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_2603}	KDNVWKISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_A909}	KDNVWKISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_CJB110}	KDNVWKISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_H36B}	KDNVWKISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_JM9130013}	KDNVWKISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_COH1}	KDNVWKISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_M781}	KDNVWKISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_M732}	KDNVWKISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_1169NT}	KDNVWKISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
Consensus	*****	*****	*****	*****	*****
	201				250
msa255178.2{91_090}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_18RS21}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_2603}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_A909}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_CJB110}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_H36B}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_JM9130013}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_COH1}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_M781}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_M732}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_1169NT}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
Consensus	*****	*****	*****	*****	*****
	251				300
msa255178.2{91_090}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TiSNETTTGF
msa255178.2{91_18RS21}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TiSNETTTGF
msa255178.2{91_2603}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TiSNETTTGF
msa255178.2{91_A909}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TiSNETTTGF
msa255178.2{91_CJB110}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TiSNETTTGF

Table 89: Comparative Sequences relating to SAG1350

msa255178.2{91_H36B}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TIsNETTTGF
msa255178.2{91_JM9130013}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TlyNETTTGF
msa255178.2{91_COH1}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TIsNETTTGF
msa255178.2{91_M781}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TIsNETTTGF
msa255178.2{91_M732}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TIsNETTTGF
msa255178.2{91_1169NT}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TIsNETTTGF
Consensus	*****	*****	*****	*****	*_*-*****
msa255178.2{91_090}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNyKVAVSFA
msa255178.2{91_18RS21}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNyKVAVSFA
msa255178.2{91_2603}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNyKVAVSFA
msa255178.2{91_A909}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNyKVAVSFA
msa255178.2{91_CJB110}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNyKVAVSFA
msa255178.2{91_H36B}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNyKVAVSFA
msa255178.2{91_JM9130013}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNyKVAVSFA
msa255178.2{91_COH1}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNyKVAVSFA
msa255178.2{91_M781}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNyKVAVSFA
msa255178.2{91_M732}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNyKVAVSFA
msa255178.2{91_1169NT}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNyKVAVSFA
Consensus	*****	*****	*****	*****	*****
msa255178.2{91_090}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTKV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_18RS21}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTKV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_2603}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTKV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_A909}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTKV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_CJB110}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTKV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_H36B}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTKV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_JM9130013}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTKV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_COH1}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTKV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_M781}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTKV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_M732}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTKV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_1169NT}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTKV	TVAGTNSSQE	PIENGLaKTG
Consensus	*****	*****	*****	*****	*****_***
msa255178.2{91_090}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_18RS21}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_2603}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_A909}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_CJB110}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_H36B}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_JM9130013}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_COH1}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_M781}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_M732}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_1169NT}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
Consensus	*****	*****	*****	*****	*****
msa255178.2{91_090}	GVRRIIPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_18RS21}	GVRRIIPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_2603}	GVRRIIPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_A909}	GVRRIIPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_CJB110}	GVRRIIPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_H36B}	GVRRIIPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_JM9130013}	GVRRIIPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_COH1}	GVRRIIPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_M781}	GVRRIIPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_M732}	GVRRIIPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_1169NT}	GVRRIIPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
Consensus	*****	*****	*****	*****	*****
msa255178.2{91_090}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_18RS21}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_2603}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_A909}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_CJB110}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_H36B}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_JM9130013}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_COH1}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_M781}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_M732}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_1169NT}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHWIS	YKSYSGIRRY	IEI
Consensus	*****	*****	*****	*****	***

CLAIMS:

1. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is
5 encoded by a GBS polynucleotide sequence which is homologous to a polynucleotide sequence of both GAS and *Streptococcus pneumoniae*.
2. The immunogenic composition of claim 1, wherein said GBS polypeptides are encoded by GBS polynucleotide sequences selected from GBS Subset 1.
3. An immunogenic composition comprising a combination of GBS polypeptides, said
10 combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS polynucleotide sequence which is homologous to a polynucleotide sequence of GAS.
4. The immunogenic composition of claim 3, wherein said GBS polypeptides are encoded by GBS polynucleotide sequences selected from GBS Subset 2.
- 15 5. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS polynucleotide sequence which is homologous to a polynucleotide sequence of *Streptococcus pneumoniae*.
6. The immunogenic composition of claim 5, wherein said GBS polypeptides are encoded
20 by GBS polynucleotide sequences selected from GBS Subset 3.
7. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS serotype polynucleotide sequence which is homologous to at least one other GBS serotype.
- 25 8. The immunogenic composition of claim 2, 4 or 6, wherein one or more of the GBS polypeptides are encoded by GBS serotype polynucleotide sequences which are homologous to at least one other GBS serotype.
9. An immunogenic composition comprising a fusion protein, wherein said fusion protein comprises a first polypeptide sequence which is encoded by a GBS serotype polynucleotide
30 which is conserved across one or more GBS serotypes.
10. A polynucleotide sequence, or a fragment comprising at least 10 contiguous polynucleotides, selected from the sequences set forth on Tables 13 – 31 and 40 – 89.
11. The polynucleotide fragment of claim 10, wherein said fragment is derived from a GBS serotype polynucleotide sequence and is homologous to at least one additional GBS serotype
35 polynucleotide sequence.

Figure 1

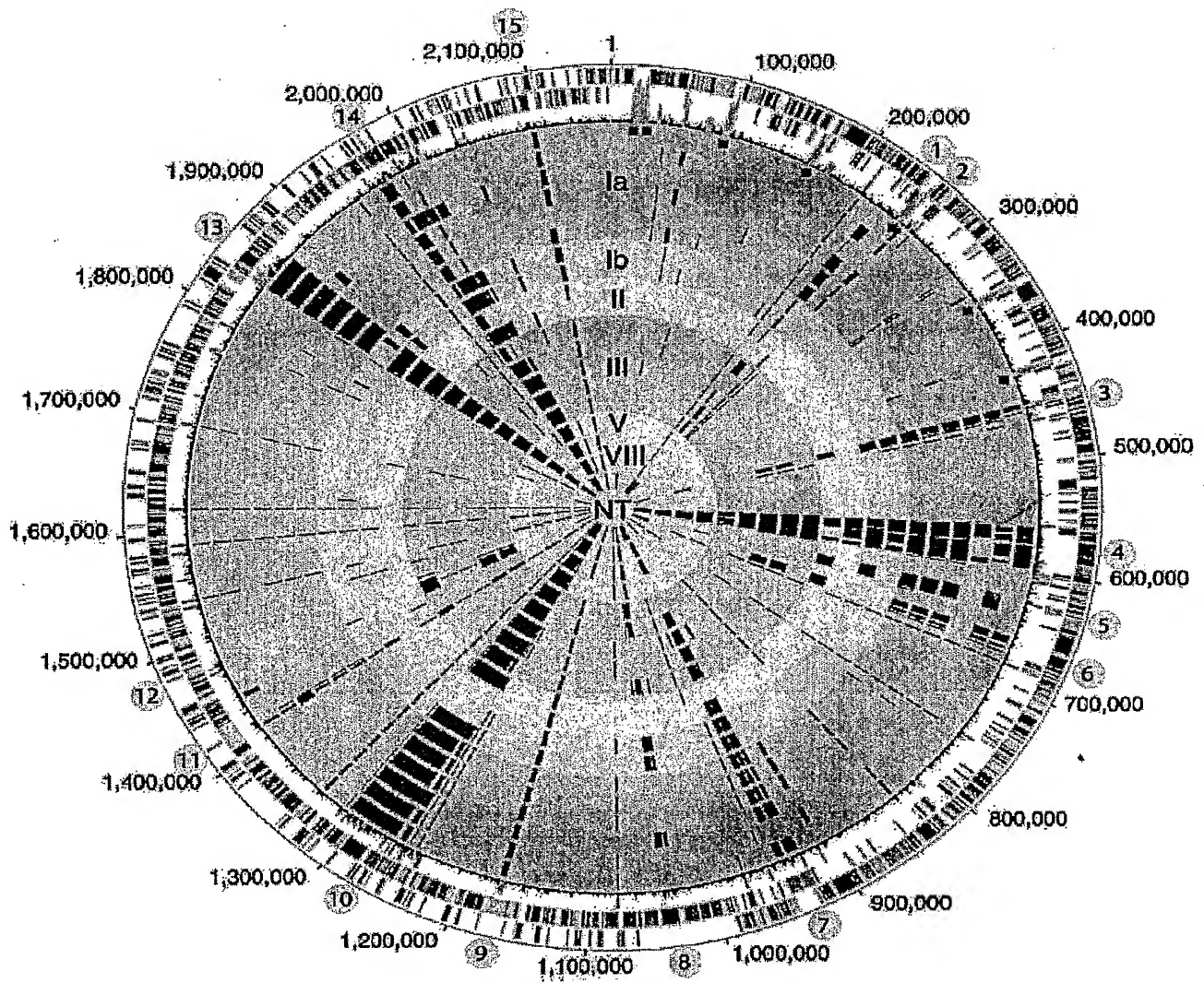


Figure 2

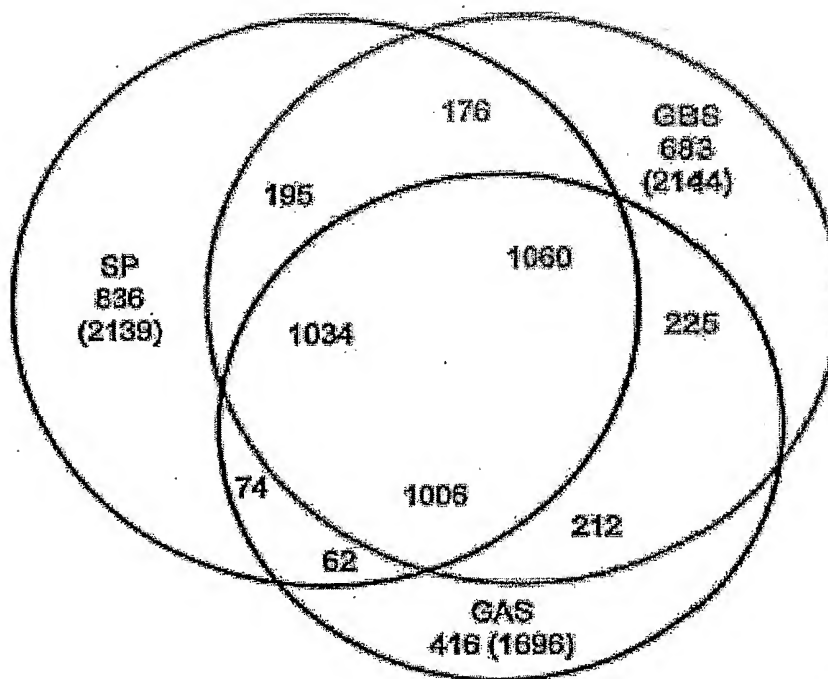
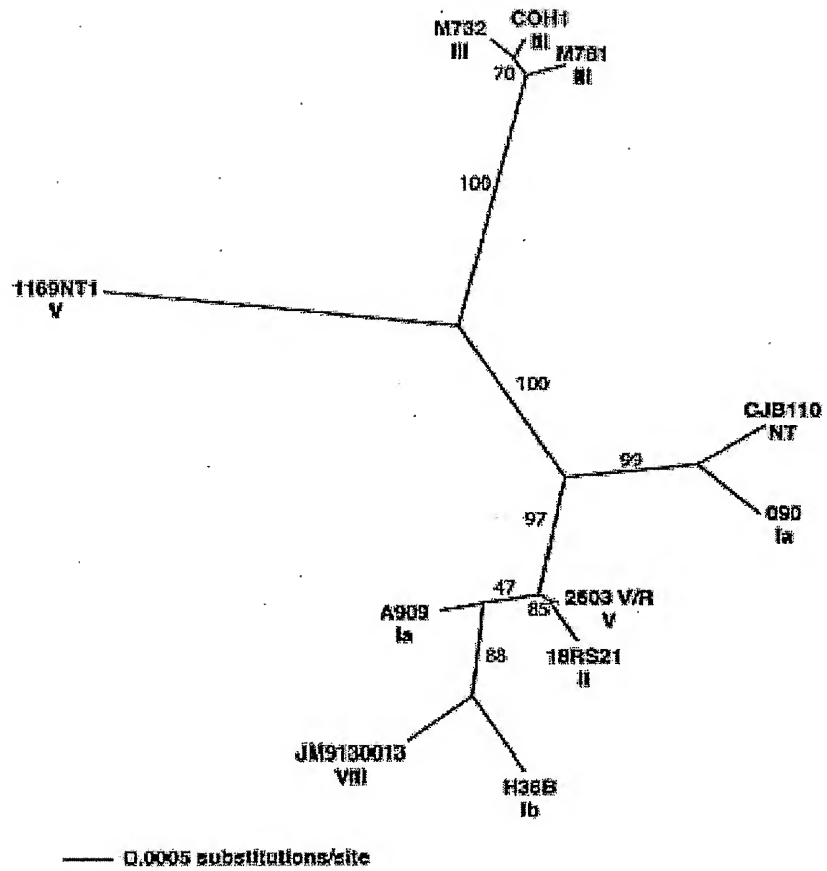


Figure 3



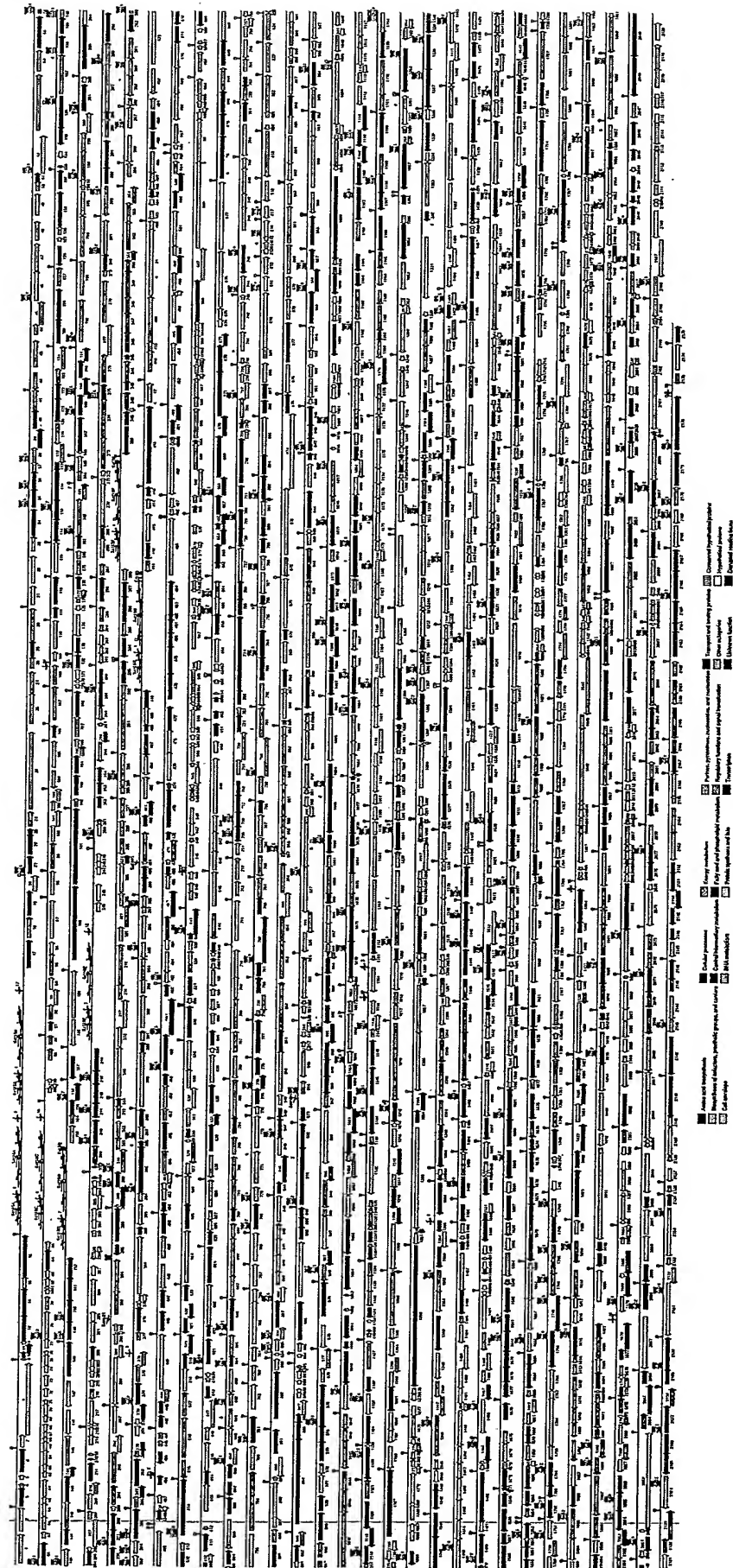


FIGURE 4

